

10/589677

SEQUENCE LISTING ~~EP 04 003 914.1~~ 16 AUG 2006

<110> Onichtchouk, Daria

<120> Use of Secreted Protein Products for Preventing and Treating
Pancreatic Diseases And/Or Obesity And/Or Metabolic Syndrome

<130> 2923-769

<150> PCT/EP2005/001711

<151> 2005-02-18

<150> EP 04 003 914.1

<151> 2004-02-20

<160> 61

<170> PatentIn version 3.3

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Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
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cag gcg gac agc gac gcg gac agc atc agc ctc gag ctg cgc aag ccc 433
Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
50 55 60
gac ggc acc ctc gtc tcc ttc acc gcc gac ttc aag aag gat gtg aag 481
Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
65 70 75 80
gtc ttc cgg gcc ctg atc ctg ggg gag ctg gag aag ggg cag agt cag 529
Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
85 90 95
ttc cag gcc ctc tgc ttt gtc acc cag ctg cag cac aat gag atc atc 577

Phe	Gln	Ala	Leu	Cys	Phe	Val	Thr	Gln	Leu	Gln	His	Asn	Glu	Ile	Ile	
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ccc	agt	gag	gcc	atg	gcc	aag	ctc	cgg	cag	aaa	aat	ccc	cgg	gca	gtg	625
Pro	Ser	Glu	Ala	Met	Ala	Lys	Leu	Arg	Gln	Lys	Asn	Pro	Arg	Ala	Val	
		115					120					125				
cgg	cag	gcg	gag	gag	gtt	cgg	ggt	ctg	gag	cat	ctg	cac	atg	gat	gtc	673
Arg	Gln	Ala	Glu	Glu	Val	Arg	Gly	Leu	Glu	His	Leu	His	Met	Asp	Val	
		130					135				140					
gct	gtc	aac	ttc	agc	cag	ggg	gcc	ctg	ctg	agc	ccc	cat	ctc	cac	aac	721
Ala	Val	Asn	Phe	Ser	Gln	Gly	Ala	Leu	Leu	Ser	Pro	His	Leu	His	Asn	
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Val	Cys	Ala	Glu	Ala	Val	Asp	Ala	Ile	Tyr	Thr	Arg	Gln	Glu	Asp	Val	
				165					170					175		
cgg	ttc	tgg	ctg	gag	caa	ggt	gtg	gac	agt	tct	gtg	ttc	gag	gct	ctg	817
Arg	Phe	Trp	Leu	Glu	Gln	Gly	Val	Asp	Ser	Ser	Val	Phe	Glu	Ala	Leu	
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Pro	Lys	Ala	Ser	Glu	Gln	Ala	Glu	Leu	Pro	Arg	Cys	Arg	Gln	Val	Gly	
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gac	cac	ggg	aag	ccc	tgc	gtc	tgc	cgc	tat	ggc	ctg	agc	ctg	gcc	tgg	913
Asp	His	Gly	Lys	Pro	Cys	Val	Cys	Arg	Tyr	Gly	Leu	Ser	Leu	Ala	Trp	
	210					215					220					
tac	ccc	tgc	atg	ctc	aag	tac	tgc	cac	agc	cgc	gac	cgg	ccc	acg	ccc	961
Tyr	Pro	Cys	Met	Leu	Lys	Tyr	Cys	His	Ser	Arg	Asp	Arg	Pro	Thr	Pro	
225					230					235					240	
tac	aag	tgt	ggc	atc	cgc	agc	tgc	cag	aag	agc	tac	agc	ttc	gac	ttc	1009
Tyr	Lys	Cys	Gly	Ile	Arg	Ser	Cys	Gln	Lys	Ser	Tyr	Ser	Phe	Asp	Phe	
				245					250					255		
tac	gtg	ccc	cag	agg	cag	ctg	tgt	ctc	tgg	gat	gag	gat	ccc	tac	cca	1057
Tyr	Val	Pro	Gln	Arg	Gln	Leu	Cys	Leu	Trp	Asp	Glu	Asp	Pro	Tyr	Pro	
			260					265					270			
ggc	taggg	tggga	gcaac	ctggc	gggt	ggctgc	tctggg	ccca	ctgctcttca							1110
Gly																
ccagcc	acta	gagggg	gtgg	caaccccc	ac	ctgagg	cctt	atttcc	cctcc	ctcccc	actc					1170
ccctgg	ccct	agagc	ctggg	cccct	ctggc	cccat	ctcac	atgact	gtga	aggggg	gtgtg					1230
gcatgg	cagg	gggt	ctcatg	aagg	cacccc	cattcc	cacc	ctgtgc	ccttc	cttg	cgggca					1290
gagaggg	gaga	gaagg	gctcc	ccagat	ctac	accc	ctcc	cctgc	atctc	ccctg	gagtg					1350

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gcatgaagta cgaggaaaac ttgaattcca gatttttagt gcaaagtatt tatcatttct 1830
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Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
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Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
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Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
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Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
65          70          75          80

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Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
85          90          95

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Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile

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100					105					110					
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	130					135					140				
Ala	Val	Asn	Phe	Ser	Gln	Gly	Ala	Leu	Leu	Ser	Pro	His	Leu	His	Asn
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Val	Cys	Ala	Glu	Ala	Val	Asp	Ala	Ile	Tyr	Thr	Arg	Gln	Glu	Asp	Val
				165					170					175	
Arg	Phe	Trp	Leu	Glu	Gln	Gly	Val	Asp	Ser	Ser	Val	Phe	Glu	Ala	Leu
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Pro	Lys	Ala	Ser	Glu	Gln	Ala	Glu	Leu	Pro	Arg	Cys	Arg	Gln	Val	Gly
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Asp	His	Gly	Lys	Pro	Cys	Val	Cys	Arg	Tyr	Gly	Leu	Ser	Leu	Ala	Trp
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Tyr	Pro	Cys	Met	Leu	Lys	Tyr	Cys	His	Ser	Arg	Asp	Arg	Pro	Thr	Pro
225					230					235					240
Tyr	Lys	Cys	Gly	Ile	Arg	Ser	Cys	Gln	Lys	Ser	Tyr	Ser	Phe	Asp	Phe
				245					250					255	
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atg gcc ggg acc gtg cgc acc gcg tgc ttg ctg gtg gcg atg ctg cta      165
Met Ala Gly Thr Val Arg Thr Ala Cys Leu Leu Val Ala Met Leu Leu
1          5          10          15

ggc ttg ggc tgc ctg gga cag gcg cag ccc ccg ccg cct cca gac gcc      213
Gly Leu Gly Cys Leu Gly Gln Ala Gln Pro Pro Pro Pro Pro Asp Ala
          20          25          30

acc tgt cac cag gtc cgt tct ttc ttc cag aga ctg cag ccc gga ctc      261
Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu Gln Pro Gly Leu
          35          40          45

aaa tgg gtt cca gaa acc cct gta cca gga tca gat ttg caa gta tgt      309
Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys
          50          55          60

ctc ccc aag ggc cca aca tgc tgc tca aga aag atg gaa gaa aaa tac      357
Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr
65          70          75          80

caa cta aca gca cgg ctg aac atg gaa caa ctg ctc cag tct gcg agt      405
Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser
          85          90          95

atg gaa ctc aag ttc tta att att cag aat gct gcg gtt ttc caa gag      453
Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu
          100          105          110

gcc ttt gaa att gtt gtt cgc cat gcc aag aac tac acc aac gcc atg      501
Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met
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ttc aag aat aac tac ccc agc ctg act cca caa gct ttt gag ttt gtc      549
Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val
          130          135          140

ggg gaa ttt ttc aca gat gtg tct ctc tac atc ttg ggt tct gat atc      597
Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile
145          150          155          160

aac gtg gat gat atg gtc aat gaa ttg ttc gac agc ctc ttt cca gtc      645
Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val
          165          170          175

atc tac acc cag atg atg aac cca ggc ctg cct gag tca gtc tta gac      693
Ile Tyr Thr Gln Met Met Asn Pro Gly Leu Pro Glu Ser Val Leu Asp
          180          185          190
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Ile Asn Glu Cys Leu Arg Gly Ala Arg Arg Asp Leu Lys Val Phe Gly	
195 200 205	
agt ttc ccc aag ctt att atg acc cag gtt tcc aag tca ctg caa gtc	789
Ser Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val	
210 215 220	
act cga atc ttc ctt caa gcc ctg aat ctc gga att gaa gtc atc aac	837
Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn	
225 230 235 240	
act acc gac cac ctc aag ttt agt aag gac tgt ggc cgt atg ctc acc	885
Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr	
245 250 255	
cga atg tgg tat tgc tct tac tgc cag gga ctg atg atg gtt aag cct	933
Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro	
260 265 270	
tgc ggt ggt tat tgc aat gtg gtc atg caa ggc tgt atg gct ggt gtg	981
Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val	
275 280 285	
gtg gag atc gac aag tac tgg aga gaa tac att ctg tct ctt gaa gag	1029
Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu	
290 295 300	
ctc gtg aat ggc atg tac aga atc tac gac atg gag aat gtg ctg ctc	1077
Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu	
305 310 315 320	
ggc ctc ttt tct acc atc cat gat tcc atc cag tat gtg cag aag aac	1125
Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn	
325 330 335	
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Gly Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln	
340 345 350	
caa cgc caa tat aga tct gct tat tac cct gaa gat ctg ttt att gac	1221
Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp	
355 360 365	
aag aag ata tta aaa gtc gct cat gtc gaa cat gaa gaa acc tta tcc	1269
Lys Lys Ile Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser	
370 375 380	
agc cga aga agg gaa ctg att cag aaa ctg aag tct ttc atc aac ttc	1317
Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Asn Phe	
385 390 395 400	
tat agc gct ttg ccg ggc tac atc tgc agc cat agc ccc gtg gcc gaa	1365
Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser Pro Val Ala Glu	

405						410						415						
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Asn	Asp	Thr	Leu	Cys	Trp	Asn	Gly	Gln	Glu	Leu	Val	Glu	Arg	Tyr	Ser			
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cag	aag	gcg	gca	agg	aac	ggg	atg	aag	aat	cag	ttt	aac	ctc	cat	gag	1461		
Gln	Lys	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His	Glu			
		435				440						445						
ctg	aaa	atg	aag	ggc	cct	gag	ccg	gtg	ggt	agc	cag	atc	att	gac	aaa	1509		
Leu	Lys	Met	Lys	Gly	Pro	Glu	Pro	Val	Val	Ser	Gln	Ile	Ile	Asp	Lys			
	450					455					460							
ctg	aag	cac	att	aac	cag	ctc	ctg	aga	acc	atg	tct	gtg	ccc	aag	ggt	1557		
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Lys	Val	Leu	Asp	Lys	Ser	Leu	Asp	Glu	Glu	Gly	Leu	Glu	Ser	Gly	Asp			
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tgc	ggt	gat	gat	gaa	gat	gaa	tgc	att	gga	agc	tct	ggt	gac	ggg	atg	1653		
Cys	Gly	Asp	Asp	Glu	Asp	Glu	Cys	Ile	Gly	Ser	Ser	Gly	Asp	Gly	Met			
			500					505					510					
gtg	aaa	gtg	aag	aat	caa	ctg	cgc	ttc	ctt	gca	gaa	ctg	gcc	tat	gat	1701		
Val	Lys	Val	Lys	Asn	Gln	Leu	Arg	Phe	Leu	Ala	Glu	Leu	Ala	Tyr	Asp			
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gac	aac	gag	atc	acc	acc	tct	cac	agc	gtg	ggg	aac	atg	ccg	tcc	cca	1797		
Asp	Asn	Glu	Ile	Thr	Thr	Ser	His	Ser	Val	Gly	Asn	Met	Pro	Ser	Pro			
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Leu	Lys	Ile	Leu	Ile	Ser	Val	Ala	Ile	Tyr	Val	Ala	Cys	Phe	Phe	Phe			
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ctg	gtg	cac	tgacttgcca	gcgtccagtg	cctgtgctgc	cctgcagcac										1894		
Leu	Val	His																
ctgtggtccc	tacagaaagg	gagccacctt	cttttttttt	tctttttttt	ttttttttta											1954		
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35 40 45

Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp Leu Gln Val Cys
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Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met Glu Glu Lys Tyr
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Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu Gln Ser Ala Ser
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Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala Val Phe Gln Glu
100 105 110

Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr Thr Asn Ala Met
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Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala Phe Glu Phe Val
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Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu Gly Ser Asp Ile
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Asn Val Asp Asp Met Val Asn Glu Leu Phe Asp Ser Leu Phe Pro Val
165 170 175

Ile Tyr Thr Gln Met Met Asn Pro Gly Leu Pro Glu Ser Val Leu Asp
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 195 200 205

Ser Phe Pro Lys Leu Ile Met Thr Gln Val Ser Lys Ser Leu Gln Val
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Thr Arg Ile Phe Leu Gln Ala Leu Asn Leu Gly Ile Glu Val Ile Asn
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Thr Thr Asp His Leu Lys Phe Ser Lys Asp Cys Gly Arg Met Leu Thr
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Arg Met Trp Tyr Cys Ser Tyr Cys Gln Gly Leu Met Met Val Lys Pro
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Cys Gly Gly Tyr Cys Asn Val Val Met Gln Gly Cys Met Ala Gly Val
 275 280 285

Val Glu Ile Asp Lys Tyr Trp Arg Glu Tyr Ile Leu Ser Leu Glu Glu
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Leu Val Asn Gly Met Tyr Arg Ile Tyr Asp Met Glu Asn Val Leu Leu
 305 310 315 320

Gly Leu Phe Ser Thr Ile His Asp Ser Ile Gln Tyr Val Gln Lys Asn
 325 330 335

Gly Gly Lys Leu Thr Thr Thr Ile Gly Lys Leu Cys Ala His Ser Gln
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Gln Arg Gln Tyr Arg Ser Ala Tyr Tyr Pro Glu Asp Leu Phe Ile Asp
 355 360 365

Lys Lys Ile Leu Lys Val Ala His Val Glu His Glu Glu Thr Leu Ser
 370 375 380

Ser Arg Arg Arg Glu Leu Ile Gln Lys Leu Lys Ser Phe Ile Asn Phe

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Gln	Lys	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His	Glu
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Leu	Lys	Met	Lys	Gly	Pro	Glu	Pro	Val	Val	Ser	Gln	Ile	Ile	Asp	Lys
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Leu	Lys	His	Ile	Asn	Gln	Leu	Leu	Arg	Thr	Met	Ser	Val	Pro	Lys	Gly
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Lys	Val	Leu	Asp	Lys	Ser	Leu	Asp	Glu	Glu	Gly	Leu	Glu	Ser	Gly	Asp
				485					490					495	
Cys	Gly	Asp	Asp	Glu	Asp	Glu	Cys	Ile	Gly	Ser	Ser	Gly	Asp	Gly	Met
			500					505					510		
Val	Lys	Val	Lys	Asn	Gln	Leu	Arg	Phe	Leu	Ala	Glu	Leu	Ala	Tyr	Asp
		515					520					525			
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	530					535					540				
Asp	Asn	Glu	Ile	Thr	Thr	Ser	His	Ser	Val	Gly	Asn	Met	Pro	Ser	Pro
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Leu	Lys	Ile	Leu	Ile	Ser	Val	Ala	Ile	Tyr	Val	Ala	Cys	Phe	Phe	Phe
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<223> SF03, cDNA: NM_004484, Protein: NP_004475

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gccgagtcct gggactgctc tcgctccggc tgccactctc ccgcgctctc ctagctccct 180
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Met Leu Leu Ser Leu Asp Phe Pro Gly Gln Ala Gln Pro Pro Pro Pro
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ccg ccg gac gcc acc tgt cac caa gtc cgc tcc ttc ttc cag aga ctg 325
Pro Pro Asp Ala Thr Cys His Gln Val Arg Ser Phe Phe Gln Arg Leu
      30              35              40              45

cag ccc gga ctc aag tgg gtg cca gaa act ccc gtg cca gga tca gat 373
Gln Pro Gly Leu Lys Trp Val Pro Glu Thr Pro Val Pro Gly Ser Asp
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ttg caa gta tgt ctc cct aag ggc cca aca tgc tgc tca aga aag atg 421
Leu Gln Val Cys Leu Pro Lys Gly Pro Thr Cys Cys Ser Arg Lys Met
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gaa gaa aaa tac caa cta aca gca cga ttg aac atg gaa cag ctg ctt 469
Glu Glu Lys Tyr Gln Leu Thr Ala Arg Leu Asn Met Glu Gln Leu Leu
          80              85              90

cag tct gca agt atg gag ctc aag ttc tta att att cag aat gct gcg 517
Gln Ser Ala Ser Met Glu Leu Lys Phe Leu Ile Ile Gln Asn Ala Ala
          95              100              105

gtt ttc caa gag gcc ttt gaa att gtt gtt cgc cat gcc aag aac tac 565
Val Phe Gln Glu Ala Phe Glu Ile Val Val Arg His Ala Lys Asn Tyr
      110              115              120              125

acc aat gcc atg ttc aag aac aac tac cca agc ctg act cca caa gct 613
Thr Asn Ala Met Phe Lys Asn Asn Tyr Pro Ser Leu Thr Pro Gln Ala
          130              135              140

ttt gag ttt gtg ggt gaa ttt ttc aca gat gtg tct ctc tac atc ttg 661
Phe Glu Phe Val Gly Glu Phe Phe Thr Asp Val Ser Leu Tyr Ile Leu
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Leu	Phe	Pro	Val	Ile	Tyr	Thr	Gln	Leu	Met	Asn	Pro	Gly	Leu	Pro	Asp		
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Ser	Ala	Leu	Asp	Ile	Asn	Glu	Cys	Leu	Arg	Gly	Ala	Arg	Arg	Asp	Leu		
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Lys	Val	Phe	Gly	Asn	Phe	Pro	Lys	Leu	Ile	Met	Thr	Gln	Val	Ser	Lys		
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Ser	Leu	Gln	Val	Thr	Arg	Ile	Phe	Leu	Gln	Ala	Leu	Asn	Leu	Gly	Ile		
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Glu	Val	Ile	Asn	Thr	Thr	Asp	His	Leu	Lys	Phe	Ser	Lys	Asp	Cys	Gly		
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Arg	Met	Leu	Thr	Arg	Met	Trp	Tyr	Cys	Ser	Tyr	Cys	Gln	Gly	Leu	Met		
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Met	Val	Lys	Pro	Cys	Gly	Gly	Tyr	Cys	Asn	Val	Val	Met	Gln	Gly	Cys		
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Met	Ala	Gly	Val	Val	Glu	Ile	Asp	Lys	Tyr	Trp	Arg	Glu	Tyr	Ile	Leu		
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Ser	Leu	Glu	Glu	Leu	Val	Asn	Gly	Met	Tyr	Arg	Ile	Tyr	Asp	Met	Glu		
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Asn	Val	Leu	Leu	Gly	Leu	Phe	Ser	Thr	Ile	His	Asp	Ser	Ile	Gln	Tyr		
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gtc	cag	aag	aat	gca	gga	aag	ctg	acc	acc	act	att	ggc	aag	tta	tgt		1237
Val	Gln	Lys	Asn	Ala	Gly	Lys	Leu	Thr	Thr	Thr	Ile	Gly	Lys	Leu	Cys		
	335					340					345						
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Ala	His	Ser	Gln	Gln	Arg	Gln	Tyr	Arg	Ser	Ala	Tyr	Tyr	Pro	Glu	Asp		
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Phe Ile Ser Phe Tyr Ser Ala Leu Pro Gly Tyr Ile Cys Ser His Ser	
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cct gtg gcg gaa aac gac acc ctt tgc tgg aat gga caa gaa ctc gtg	1477
Pro Val Ala Glu Asn Asp Thr Leu Cys Trp Asn Gly Gln Glu Leu Val	
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Glu Arg Tyr Ser Gln Lys Ala Ala Arg Asn Gly Met Lys Asn Gln Phe	
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Asn Leu His Glu Leu Lys Met Lys Gly Pro Glu Pro Val Val Ser Gln	
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Ile Ile Asp Lys Leu Lys His Ile Asn Gln Leu Leu Arg Thr Met Ser	
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Met Pro Lys Gly Arg Val Leu Asp Lys Asn Leu Asp Glu Glu Gly Phe	
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Glu Ser Gly Asp Cys Gly Asp Asp Glu Asp Glu Cys Ile Gly Gly Ser	
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Ala Thr Pro Lys Asp Asn Glu Ile Ser Thr Phe His Asn Leu Gly Asn	
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Val His Ser Pro Leu Lys Leu Leu Thr Ser Met Ala Ile Ser Val Val	
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Cys Phe Phe Phe Leu Val His	
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Ala	Thr	Cys	His	Gln	Val	Arg	Ser	Phe	Phe	Gln	Arg	Leu	Gln	Pro	Gly	
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Leu	Lys	Trp	Val	Pro	Glu	Thr	Pro	Val	Pro	Gly	Ser	Asp	Leu	Gln	Val	
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Cys	Leu	Pro	Lys	Gly	Pro	Thr	Cys	Cys	Ser	Arg	Lys	Met	Glu	Glu	Lys	
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Tyr	Gln	Leu	Thr	Ala	Arg	Leu	Asn	Met	Glu	Gln	Leu	Leu	Gln	Ser	Ala	
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Ser	Met	Glu	Leu	Lys	Phe	Leu	Ile	Ile	Gln	Asn	Ala	Ala	Val	Phe	Gln	
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Ile	Asn	Val	Asp	Asp	Met	Val	Asn	Glu	Leu	Phe	Asp	Ser	Leu	Phe	Pro	165	170	175	
Val	Ile	Tyr	Thr	Gln	Leu	Met	Asn	Pro	Gly	Leu	Pro	Asp	Ser	Ala	Leu	180	185	190	
Asp	Ile	Asn	Glu	Cys	Leu	Arg	Gly	Ala	Arg	Arg	Asp	Leu	Lys	Val	Phe	195	200	205	
Gly	Asn	Phe	Pro	Lys	Leu	Ile	Met	Thr	Gln	Val	Ser	Lys	Ser	Leu	Gln	210	215	220	
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Thr	Arg	Met	Trp	Tyr	Cys	Ser	Tyr	Cys	Gln	Gly	Leu	Met	Met	Val	Lys	260	265	270	
Pro	Cys	Gly	Gly	Tyr	Cys	Asn	Val	Val	Met	Gln	Gly	Cys	Met	Ala	Gly	275	280	285	
Val	Val	Glu	Ile	Asp	Lys	Tyr	Trp	Arg	Glu	Tyr	Ile	Leu	Ser	Leu	Glu	290	295	300	
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Leu	Gly	Leu	Phe	Ser	Thr	Ile	His	Asp	Ser	Ile	Gln	Tyr	Val	Gln	Lys	325	330	335	
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Ser	Ser	Arg	Arg	Arg	Glu	Leu	Ile	Gln	Lys	Leu	Lys	Ser	Phe	Ile	Ser				
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Ser	Gln	Lys	Ala	Ala	Arg	Asn	Gly	Met	Lys	Asn	Gln	Phe	Asn	Leu	His				
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Lys	Leu	Lys	His	Ile	Asn	Gln	Leu	Leu	Arg	Thr	Met	Ser	Met	Pro	Lys				
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Lys	Asp	Asn	Glu	Ile	Ser	Thr	Phe	His	Asn	Leu	Gly	Asn	Val	His	Ser				
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<223> SF04, cDNA: NM_007443, Protein: NP_031469

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ctg ctg ctg act gcc tgc ctc gct tgc agg gct gac cct gcg tca aca      160
Leu Leu Leu Thr Ala Cys Leu Ala Ser Arg Ala Asp Pro Ala Ser Thr
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ctg cca gat atc cag gtt cag gag aac ttc agt gag tcc cgg atc tat      208
Leu Pro Asp Ile Gln Val Gln Glu Asn Phe Ser Glu Ser Arg Ile Tyr
    25                      30                      35                      40

gga aaa tgg tac aac ctg gcg gtg gga tcc acc tgc ccg tgg ctg agc      256
Gly Lys Trp Tyr Asn Leu Ala Val Gly Ser Thr Cys Pro Trp Leu Ser
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cgc att aag gac aag atg agc gtg agc acg ctg gtg ctg cag gag ggg      304
Arg Ile Lys Asp Lys Met Ser Val Ser Thr Leu Val Leu Gln Glu Gly
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gcg aca gaa aca gag atc agc atg acc agt act cga tgg cgg aga ggt      352
Ala Thr Glu Thr Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Arg Gly
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Val Cys Glu Glu Ile Thr Gly Ala Tyr Gln Lys Thr Asp Ile Asp Gly
    90                      95                      100

aag ttc ctc tac cac aaa tcc aaa tgg aac ata acc ttg gaa tcc tat      448
Lys Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Leu Glu Ser Tyr
    105                      110                      115                      120

gtg gtc cac acc aac tat gac gaa tat gcc att ttc ctt acc aag aag      496
Val Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys
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tcc agc cac cac cac ggg ctc acc atc act gcc aag ctc tat ggt cgg      544

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Glu	Pro	Gln	Leu	Arg	Asp	Ser	Leu	Leu	Gln	Glu	Phe	Lys	Asp	Val	Ala		
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Leu	Asn	Val	Gly	Ile	Ser	Glu	Asn	Ser	Ile	Ile	Phe	Met	Pro	Asp	Arg		
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Gly	Glu	Cys	Val	Pro	Gly	Asp	Arg	Glu	Val	Glu	Pro	Thr	Ser	Ile	Ala		
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Arg	Ala	Arg	Arg	Ala	Val	Leu	Pro	Gln	Glu	Ser	Glu	Gly	Ser	Gly	Thr		
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Glu	Pro	Leu	Ile	Thr	Gly	Thr	Leu	Lys	Lys	Glu	Asp	Ser	Cys	Gln	Leu		
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Asn	Tyr	Ser	Glu	Gly	Pro	Cys	Leu	Gly	Met	Gln	Glu	Arg	Tyr	Tyr	Tyr		
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Asn	Gly	Ala	Ser	Met	Ala	Cys	Glu	Thr	Phe	Gln	Tyr	Gly	Gly	Cys	Leu		
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Arg	Thr	Ile	Ala	Ala	Cys	Asn	Leu	Pro	Ile	Val	Gln	Gly	Pro	Cys	Arg		
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gcc	ttc	ata	aag	ctc	tgg	gca	ttt	gat	gca	gca	caa	ggg	aag	tgc	atc	1024	
Ala	Phe	Ile	Lys	Leu	Trp	Ala	Phe	Asp	Ala	Ala	Gln	Gly	Lys	Cys	Ile		
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Gln	Phe	His	Tyr	Gly	Gly	Cys	Lys	Gly	Asn	Gly	Asn	Lys	Phe	Tyr	Ser		
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 35 40 45

Gly Ser Thr Cys Pro Trp Leu Ser Arg Ile Lys Asp Lys Met Ser Val
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Ser Thr Leu Val Leu Gln Glu Gly Ala Thr Glu Thr Glu Ile Ser Met
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Thr Ser Thr Arg Trp Arg Arg Gly Val Cys Glu Glu Ile Thr Gly Ala
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Trp Asn Ile Thr Leu Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu
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Ile Thr Ala Lys Leu Tyr Gly Arg Glu Pro Gln Leu Arg Asp Ser Leu
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Ser Ile Ile Phe Met Pro Asp Arg Gly Glu Cys Val Pro Gly Asp Arg

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Met Arg Ser	
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Leu Gly Ala Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser Ala	
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Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn Phe	
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Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly Ser	
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Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser Thr	
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Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr Ser	
70 75 80	
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Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly Ala Tyr Glu	
85 90 95	
aaa aca gat act gat ggg aag ttt ctc tat cac aaa tcc aaa tgg aac	571
Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser Lys Trp Asn	
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Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr Leu Leu Gln	
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Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr
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Phe Asp Ala Val Lys Gly Lys Cys Val Leu Phe Pro Tyr Gly Gly Cys		
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Gln	Tyr	Val	Met	Lys	Leu	Ala	Asn	Ser	Leu	Phe	Val	Gln	Asn	Gly	Phe	
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Trp	Ala	Asn	Ser	Val	Lys	Lys	Gln	Lys	Val	Glu	Val	Tyr	Leu	Pro	Arg		
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Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
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aaa aaa tat ttt aat gca gca gta aat cat gtg gac ttc agt caa aat      852
Lys Lys Tyr Phe Asn Ala Ala Val Asn His Val Asp Phe Ser Gln Asn
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Tyr Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser	
180 185 190	
cag ttt agg cct gaa aat act aga acc ttt tct ttc act aaa gat gat	1044
Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp	
195 200 205	
gaa agt gaa gtc caa att cca atg atg tat cag caa gga gaa ttt tat	1092
Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr	
210 215 220	
tat ggg gaa ttt agt gat ggc tcc aat gaa gct ggt ggt atc tac caa	1140
Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln	
225 230 235 240	
gtc cta gaa ata cca tat gaa gga gat gaa ata agc atg atg ctg gtg	1188
Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Val	
245 250 255	
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Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Val Lys	
260 265 270	
gca cag ctg gtt gaa gaa tgg gca aac tct gtg aag aag caa aaa gta	1284
Ala Gln Leu Val Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val	
275 280 285	
gaa gta tac ctg ccc agg ttc aca gtg gaa cag gaa att gat tta aaa	1332
Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys	
290 295 300	
gat gtt ttg aag gct ctt gga ata act gaa att ttc atc aaa gat gca	1380
Asp Val Leu Lys Ala Leu Gly Ile Thr Glu Ile Phe Ile Lys Asp Ala	
305 310 315 320	
aat ttg aca ggc ctc tct gat aat aag gag att ttt ctt tcc aaa gca	1428
Asn Leu Thr Gly Leu Ser Asp Asn Lys Glu Ile Phe Leu Ser Lys Ala	
325 330 335	
att cac aag tcc ttc cta gag gtt aat gaa gaa ggc tca gaa gct gct	1476
Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala	
340 345 350	
gct gtc tca gga atg att gca att agt agg atg gct gtg ctg tat cct	1524
Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro	
355 360 365	

caa gtt att gtc gac cat cca ttt ttc ttt ctt atc aga aac agg aga	1572
Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg	
370 375 380	

act ggt aca att cta ttc atg gga cga gtc atg cat cct gaa aca atg	1620
Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met	
385 390 395 400	

aac aca agt gga cat gat ttc gaa gaa ctt taagttactt tatttgaata	1670
Asn Thr Ser Gly His Asp Phe Glu Glu Leu	
405 410	

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attataagta acttgtcaag gaatgttatc agtattaagc taatggtcct gttatgtcat	1850
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<212> PRT

<213> Homo sapiens

<400> 29

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Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe
35 40 45

Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
50 55 60

Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser
65 70 75 80

Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
85 90 95

Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu
100 105 110

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Lys	Lys	Tyr	Phe	Asn	Ala	Ala	Val	Asn	His	Val	Asp	Phe	Ser	Gln	Asn		
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Tyr	Leu	Ala	Leu	Ile	Asn	Ala	Val	Tyr	Phe	Lys	Gly	Asn	Trp	Lys	Ser		
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Gln	Phe	Arg	Pro	Glu	Asn	Thr	Arg	Thr	Phe	Ser	Phe	Thr	Lys	Asp	Asp		
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Glu	Ser	Glu	Val	Gln	Ile	Pro	Met	Met	Tyr	Gln	Gln	Gly	Glu	Phe	Tyr		
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Tyr	Gly	Glu	Phe	Ser	Asp	Gly	Ser	Asn	Glu	Ala	Gly	Gly	Ile	Tyr	Gln		
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Glu	Val	Tyr	Leu	Pro	Arg	Phe	Thr	Val	Glu	Gln	Glu	Ile	Asp	Leu	Lys		
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325	330	335
Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala		
340	345	350
Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro		
355	360	365
Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg		
370	375	380
Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met		
385	390	395
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Asn Thr Ser Gly His Asp Phe Glu Glu Leu		
405	410	

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 <223> SF06, cDNA: NM_172633, Protein: NP_766221

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Pro Leu Leu Ser Met Pro Gly Arg Arg Gly Ala Leu Arg Glu Pro Ala	
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gac ttt ggc tcc agc ctg ggg gcg gtg ctg gcc ctg ctg ttg ctg ctg	148
Asp Phe Gly Ser Ser Leu Gly Ala Val Leu Ala Leu Leu Leu Leu	
30 35 40	
ctg ccc gcc tgc tgc ccc gta agg gct cag aac gac acg gag ccc atc	196
Leu Pro Ala Cys Cys Pro Val Arg Ala Gln Asn Asp Thr Glu Pro Ile	
45 50 55	
gtg cta gag ggc aag tgc ctg gta gtg tgc gat tcc agc cca tcg ggg	244
Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp Ser Ser Pro Ser Gly	
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Asp Gly Ala Val Thr Ser Ser Leu Gly Ile Ser Val Arg Ser Gly Ser	
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gcc aag gtg gcc ttc tcc gct act cgg agc acc aac cac gag ccg tca	340
Ala Lys Val Ala Phe Ser Ala Thr Arg Ser Thr Asn His Glu Pro Ser	
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gag atg agc aac cgt acc atg acc atc tac ttc gac cag gtc tta gta	388
Glu Met Ser Asn Arg Thr Met Thr Ile Tyr Phe Asp Gln Val Leu Val	
110 115 120	
aac att ggc aac cac ttt gac ctt gcc tcc agt ata ttt gta gca cca	436
Asn Ile Gly Asn His Phe Asp Leu Ala Ser Ser Ile Phe Val Ala Pro	
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Arg Lys Gly Ile Tyr Ser Phe Ser Phe His Val Val Lys Val Tyr Asn	
140 145 150	
aga caa act atc cag gtc agc tta atg cag aat ggc tac ccg gtg atc	532
Arg Gln Thr Ile Gln Val Ser Leu Met Gln Asn Gly Tyr Pro Val Ile	
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tct gca ttt gcc gga gac cag gat gtt acc agg gaa gca gcc agc aat	580
Ser Ala Phe Ala Gly Asp Gln Asp Val Thr Arg Glu Ala Ala Ser Asn	
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ggt gtt ctg ctg ctc atg gaa aga gaa gac aaa gtt cat ctc aaa cta	628
Gly Val Leu Leu Leu Met Glu Arg Glu Asp Lys Val His Leu Lys Leu	
190 195 200	
gag aga ggc aac ctc atg gga ggc tgg aaa tac tcc aca ttc tcg ggc	676
Glu Arg Gly Asn Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly	
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Phe Leu Val Phe Pro Leu	
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<212> PRT
<213> Mus musculus

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<400> 31

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          20          25          30

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Gly Ala Val Leu Ala Leu Leu Leu Leu Leu Pro Ala Cys Cys Pro
          35          40          45

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Val Arg Ala Gln Asn Asp Thr Glu Pro Ile Val Leu Glu Gly Lys Cys
50 55 60

Leu Val Val Cys Asp Ser Ser Pro Ser Gly Asp Gly Ala Val Thr Ser
65 70 75 80

Ser Leu Gly Ile Ser Val Arg Ser Gly Ser Ala Lys Val Ala Phe Ser
85 90 95

Ala Thr Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Arg Thr
100 105 110

Met Thr Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn His Phe
115 120 125

Asp Leu Ala Ser Ser Ile Phe Val Ala Pro Arg Lys Gly Ile Tyr Ser
130 135 140

Phe Ser Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile Gln Val
145 150 155 160

Ser Leu Met Gln Asn Gly Tyr Pro Val Ile Ser Ala Phe Ala Gly Asp
165 170 175

Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Leu Leu Met
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Glu Arg Glu Asp Lys Val His Leu Lys Leu Glu Arg Gly Asn Leu Met
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Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe Pro Leu
210 215 220

<210> 32
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<213> Homo sapiens

<220>
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<223> SF06, cDNA: NM_182511, Protein: NP_872317

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cgcgccgcct cccaccagtc ccg atg cag gcg ccc ggc cg ggg cca ctc ggg 593

Met Gln Ala Pro Gly Arg Gly Pro Leu Gly

1 5 10

ctg cg gctg atg atg ccc ggg cgc cg ggg gcg ctg cgc gag cct ggc 641

Leu Arg Leu Met Met Pro Gly Arg Arg Gly Ala Leu Arg Glu Pro Gly

15 20 25

ggc tgc gga tcc tgc ctg ggg gtg gcg ctg gcc ctg ctg ttg ctg cta 689

Gly Cys Gly Ser Cys Leu Gly Val Ala Leu Ala Leu Leu Leu Leu Leu

30 35 40

ctg ccc gcc tgc tgc ccc gtg cgg gcg cag aac gac acg gag ccc atc 737

Leu Pro Ala Cys Cys Pro Val Arg Ala Gln Asn Asp Thr Glu Pro Ile

45 50 55

gtg ctg gag ggc aag tgc ctg gtg gtg tgc gac tcc agc ccg tcg gcg 785

Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp Ser Ser Pro Ser Ala

60 65 70

gac ggc gcc gtc acc tcc tcc cta ggc atc tcc gtg cgc tcc ggc agc 833

Asp Gly Ala Val Thr Ser Ser Leu Gly Ile Ser Val Arg Ser Gly Ser

75 80 85 90

gcc aag gtg gcc ttc tcc gcc acg cgg agc acc aac cac gag ccg tcc 881

Ala Lys Val Ala Phe Ser Ala Thr Arg Ser Thr Asn His Glu Pro Ser

95 100 105

gag atg agc aac cgc acc atg acc atc tat ttc gac cag gta tta gta 929

Glu Met Ser Asn Arg Thr Met Thr Ile Tyr Phe Asp Gln Val Leu Val

110 115 120

aat att ggc aac cac ttt gat ctt gct tcc agt ata ttt gta gca ccg 977

Asn Ile Gly Asn His Phe Asp Leu Ala Ser Ser Ile Phe Val Ala Pro

125 130 135

aga aaa ggg att tat agc ttc agc ttc cac gtg gtc aaa gtg tat aac	1025
Arg Lys Gly Ile Tyr Ser Phe Ser Phe His Val Val Lys Val Tyr Asn	
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Arg Gln Thr Ile Gln Val Ser Leu Met Gln Asn Gly Tyr Pro Val Ile	
155 160 165 170	
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175 180 185	
ggc gtg ctg ctg ctc atg gaa agg gaa gac aaa gtg cat ctc aaa ctt	1169
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190 195 200	
gag aga ggc aac ctc atg ggg ggc tgg aaa tac tcc aca ttc tcg ggc	1217
Glu Arg Gly Asn Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly	
205 210 215	
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Phe Leu Val Phe Pro Leu	
220	
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<210> 33
<211> 224
<212> PRT
<213> Homo sapiens

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Gly Arg Arg Gly Ala Leu Arg Glu Pro Gly Gly Cys Gly Ser Cys Leu
          20          25          30

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Gly Val Ala Leu Ala Leu Leu Leu Leu Leu Leu Pro Ala Cys Cys Pro
          35          40          45

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Val Arg Ala Gln Asn Asp Thr Glu Pro Ile Val Leu Glu Gly Lys Cys
50          55          60

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Leu Val Val Cys Asp Ser Ser Pro Ser Ala Asp Gly Ala Val Thr Ser
65          70          75          80

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```

Ser Leu Gly Ile Ser Val Arg Ser Gly Ser Ala Lys Val Ala Phe Ser
          85          90          95

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Ala Thr Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Arg Thr
          100          105          110

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Met Thr Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn His Phe
 115 120 125

Asp Leu Ala Ser Ser Ile Phe Val Ala Pro Arg Lys Gly Ile Tyr Ser
 130 135 140

Phe Ser Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile Gln Val
 145 150 155 160

Ser Leu Met Gln Asn Gly Tyr Pro Val Ile Ser Ala Phe Ala Gly Asp
 165 170 175

Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Leu Leu Met
 180 185 190

Glu Arg Glu Asp Lys Val His Leu Lys Leu Glu Arg Gly Asn Leu Met
 195 200 205

Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe Pro Leu
 210 215 220

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 <211> 1542
 <212> DNA
 <213> Mus musculus

<220>
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 <223> SF07, cDNA: NM_026840, Protein: NP_081116

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 agccctgaag atg aag ttt tgg ctg ctg ctc gga ctt ctg ttg cta cac 169
 Met Lys Phe Trp Leu Leu Leu Gly Leu Leu Leu Leu His
 1 5 10
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 Glu Ala Leu Glu Asp Val Ala Gly Gln His Ser Pro Lys Asn Lys Arg
 15 20 25
 cca aag gag caa gga gaa aac aga atc aaa cca acc aac aaa aag gcc 265
 Pro Lys Glu Gln Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Ala
 30 35 40 45

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110					115					120					125	
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Gly	Gln	Leu	Thr	Leu	Val	Asn	Ser	Thr	Ala	Ala	Asp	Thr	Gly	Glu	Phe	
				130					135					140		
agc	tgc	tgg	gag	caa	ctg	tgc	aat	ggc	tac	atc	tgc	aga	cgg	gat	gaa	601
Ser	Cys	Trp	Glu	Gln	Leu	Cys	Asn	Gly	Tyr	Ile	Cys	Arg	Arg	Asp	Glu	
			145					150					155			
gcc	aaa	aca	ggc	tcc	acc	tat	atc	ttc	ttc	aca	gag	aaa	gga	gag	ctg	649
Ala	Lys	Thr	Gly	Ser	Thr	Tyr	Ile	Phe	Phe	Thr	Glu	Lys	Gly	Glu	Leu	
		160					165					170				
ttt	gtg	cct	tct	ccc	agt	tac	ttt	gat	gtt	gtc	tac	ctg	aac	ccg	gac	697
Phe	Val	Pro	Ser	Pro	Ser	Tyr	Phe	Asp	Val	Val	Tyr	Leu	Asn	Pro	Asp	
	175					180					185					
aga	caa	gct	gtg	gtt	cct	tgt	cga	gtg	aca	gcc	cca	tca	gcc	aaa	gtc	745
Arg	Gln	Ala	Val	Val	Pro	Cys	Arg	Val	Thr	Ala	Pro	Ser	Ala	Lys	Val	
190					195				200						205	
acg	ctc	cac	agg	gag	ttt	ccc	gcc	aaa	gaa	atc	cct	gcc	aat	ggc	acg	793
Thr	Leu	His	Arg	Glu	Phe	Pro	Ala	Lys	Glu	Ile	Pro	Ala	Asn	Gly	Thr	
				210					215					220		
gac	att	gtg	tac	gac	atg	aag	aga	ggg	ttc	gtg	tac	ctt	cag	cct	cat	841
Asp	Ile	Val	Tyr	Asp	Met	Lys	Arg	Gly	Phe	Val	Tyr	Leu	Gln	Pro	His	
			225					230					235			
tcc	gat	cac	cag	ggg	gtg	gtc	tac	tgc	aaa	gcg	gaa	gcc	ggg	ggc	aag	889
Ser	Asp	His	Gln	Gly	Val	Val	Tyr	Cys	Lys	Ala	Glu	Ala	Gly	Gly	Lys	
		240					245					250				
tct	cag	atc	tca	gtc	aag	tat	cag	ctg	ctc	tat	gta	gag	gtt	cct	agt	937
Ser	Gln	Ile	Ser	Val	Lys	Tyr	Gln	Leu	Leu	Tyr	Val	Glu	Val	Pro	Ser	

255	260	265	
ggc cct cca tca aca acc atc ttg gcc tcc tct aac aaa gtg agg ggc			985
Gly Pro Pro Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Arg Gly			
270	275	280	285
ggt gat gac atc agc gtg ctc tgc act gtc ctc ggg gag cct gat gtg			1033
Gly Asp Asp Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val			
	290	295	300
gag gtt gaa ttc agg tgg ctc ttt cct ggg cag aag gac gaa agg cct			1081
Glu Val Glu Phe Arg Trp Leu Phe Pro Gly Gln Lys Asp Glu Arg Pro			
	305	310	315
gtg acc atc cag gac acc tgg aga ctg att cac aga gga ctg gga cac			1129
Val Thr Ile Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His			
	320	325	330
acc aca aga atc tcc cag agt gtc att atc gtg gaa gac ttt gag acc			1177
Thr Thr Arg Ile Ser Gln Ser Val Ile Ile Val Glu Asp Phe Glu Thr			
	335	340	345
att gat gcg ggc tac tac ata tgc aca gct cag aat ctc cga gga cag			1225
Ile Asp Ala Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Arg Gly Gln			
350	355	360	365
acc aca gta gcg acc act gtt gag ttt tcc tgattggaaa gtgaagagta			1275
Thr Thr Val Ala Thr Thr Val Glu Phe Ser			
	370	375	
gtggaccaat gggatgccca tctgcacaca cagcttccag gtgctttata ggaggccaag			1335
ggccaacccc tgccagtggg tcagacagac atccgaatta aaaggaagtc actagtctat			1395
taatagaagt ataaactttc ctaactaaag tatgtatttt gactcagcca tgtttctact			1455
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attttataaa aaaaaaaaaa aaaaaaa			1542

<210> 35
 <211> 375
 <212> PRT
 <213> Mus musculus

<400> 35

Met	Lys	Phe	Trp	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Leu	His	Glu	Ala	Leu
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Glu	Asp	Val	Ala	Gly	Gln	His	Ser	Pro	Lys	Asn	Lys	Arg	Pro	Lys	Glu
			20					25					30		

Gln	Gly	Glu	Asn	Arg	Ile	Lys	Pro	Thr	Asn	Lys	Lys	Ala	Lys	Pro	Lys			
		35					40					45						
Ile	Pro	Lys	Val	Lys	Asp	Arg	Asp	Ser	Thr	Asp	Ser	Thr	Ala	Lys	Ser			
	50					55					60							
Gln	Ser	Ile	Met	Met	Gln	Ala	Met	Gly	Asn	Gly	Arg	Phe	Gln	Arg	Pro			
65					70					75					80			
Ala	Ala	Thr	Val	Ser	Leu	Leu	Ala	Gly	Gln	Thr	Leu	Glu	Leu	Arg	Cys			
				85					90					95				
Lys	Gly	Ser	Lys	Val	Glu	Trp	Ser	Tyr	Pro	Ala	Tyr	Leu	Asp	Thr	Phe			
			100					105					110					
Lys	Asp	Ser	Arg	Leu	Thr	Val	Lys	Gln	Ser	Glu	Arg	Tyr	Gly	Gln	Leu			
		115					120						125					
Thr	Leu	Val	Asn	Ser	Thr	Ala	Ala	Asp	Thr	Gly	Glu	Phe	Ser	Cys	Trp			
	130					135					140							
Glu	Gln	Leu	Cys	Asn	Gly	Tyr	Ile	Cys	Arg	Arg	Asp	Glu	Ala	Lys	Thr			
145					150					155					160			
Gly	Ser	Thr	Tyr	Ile	Phe	Phe	Thr	Glu	Lys	Gly	Glu	Leu	Phe	Val	Pro			
				165					170					175				
Ser	Pro	Ser	Tyr	Phe	Asp	Val	Val	Tyr	Leu	Asn	Pro	Asp	Arg	Gln	Ala			
			180					185					190					
Val	Val	Pro	Cys	Arg	Val	Thr	Ala	Pro	Ser	Ala	Lys	Val	Thr	Leu	His			
		195					200					205						
Arg	Glu	Phe	Pro	Ala	Lys	Glu	Ile	Pro	Ala	Asn	Gly	Thr	Asp	Ile	Val			
	210					215					220							
Tyr	Asp	Met	Lys	Arg	Gly	Phe	Val	Tyr	Leu	Gln	Pro	His	Ser	Asp	His			
225					230					235					240			
Gln	Gly	Val	Val	Tyr	Cys	Lys	Ala	Glu	Ala	Gly	Gly	Lys	Ser	Gln	Ile			
				245					250					255				

Ser Val Lys Tyr Gln Leu Leu Tyr Val Glu Val Pro Ser Gly Pro Pro
260 265 270

Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Arg Gly Gly Asp Asp
275 280 285

Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu
290 295 300

Phe Arg Trp Leu Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile
305 310 315 320

Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg
325 330 335

Ile Ser Gln Ser Val Ile Ile Val Glu Asp Phe Glu Thr Ile Asp Ala
340 345 350

Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Arg Gly Gln Thr Thr Val
355 360 365

Ala Thr Thr Val Glu Phe Ser
370 375

<210> 36
<211> 1502
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (62)..(1186)
<223> SF07, cDNA: NM_006207, Protein: NP_006198

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g atg aag gtc tgg ctg ctg ctt ggt ctt ctg ctg gtg cac gaa gcg ctg 109
Met Lys Val Trp Leu Leu Leu Gly Leu Leu Val His Glu Ala Leu
1 5 10 15
gag gat gtt act ggc caa cac ctt ccc aag aac aag cgt cca aaa gaa 157
Glu Asp Val Thr Gly Gln His Leu Pro Lys Asn Lys Arg Pro Lys Glu
20 25 30

cca gga gag aat aga atc aaa cct acc aac aag aag gtg aag ccc aaa	205
Pro Gly Glu Asn Arg Ile Lys Pro Thr Asn Lys Lys Val Lys Pro Lys	
35 40 45	
att cct aaa atg aag gac agg gac tca gcc aat tca gca cca aag acg	253
Ile Pro Lys Met Lys Asp Arg Asp Ser Ala Asn Ser Ala Pro Lys Thr	
50 55 60	
cag tct atc atg atg caa gtg ctg gat aaa ggt cgc ttc cag aaa ccc	301
Gln Ser Ile Met Met Gln Val Leu Asp Lys Gly Arg Phe Gln Lys Pro	
65 70 75 80	
gcc gct acc ctg agt ctg ctg gcg ggg caa act gta gag ctt cga tgt	349
Ala Ala Thr Leu Ser Leu Leu Ala Gly Gln Thr Val Glu Leu Arg Cys	
85 90 95	
aaa ggg agt aga att ggg tgg agc tac cct gcg tat ctg gac acc ttt	397
Lys Gly Ser Arg Ile Gly Trp Ser Tyr Pro Ala Tyr Leu Asp Thr Phe	
100 105 110	
aag gat tct cgc ctc agc gtc aag cag aat gag cgc tac ggc cag ttg	445
Lys Asp Ser Arg Leu Ser Val Lys Gln Asn Glu Arg Tyr Gly Gln Leu	
115 120 125	
act ctg gtc aac tcc acc tcg gca gac aca ggt gaa ttc agc tgc tgg	493
Thr Leu Val Asn Ser Thr Ser Ala Asp Thr Gly Glu Phe Ser Cys Trp	
130 135 140	
gtg cag ctc tgc agc ggc tac atc tgc agg aag gac gag gcc aaa acg	541
Val Gln Leu Cys Ser Gly Tyr Ile Cys Arg Lys Asp Glu Ala Lys Thr	
145 150 155 160	
ggc tcc acc tac atc ttt ttt aca gag aaa gga gaa ctc ttt gta cct	589
Gly Ser Thr Tyr Ile Phe Phe Thr Glu Lys Gly Glu Leu Phe Val Pro	
165 170 175	
tct ccc agc tac ttc gat gtt gtc tac ttg aac ccg gac aga cag gct	637
Ser Pro Ser Tyr Phe Asp Val Val Tyr Leu Asn Pro Asp Arg Gln Ala	
180 185 190	
gtg gtt cct tgt cgg gtg acc gtg ctg tcg gcc aaa gtc acg ctc cac	685
Val Val Pro Cys Arg Val Thr Val Leu Ser Ala Lys Val Thr Leu His	
195 200 205	
agg gaa ttc cca gcc aag gag atc cca gcc aat gga acg gac att gtt	733
Arg Glu Phe Pro Ala Lys Glu Ile Pro Ala Asn Gly Thr Asp Ile Val	
210 215 220	
tat gac atg aag cgg ggc ttt gtg tat ctg caa cct cat tcc gag cac	781
Tyr Asp Met Lys Arg Gly Phe Val Tyr Leu Gln Pro His Ser Glu His	
225 230 235 240	
cag ggt gtg gtt tac tgc agg gcg gag gcc ggg ggc aga tct cag atc	829
Gln Gly Val Val Tyr Cys Arg Ala Glu Ala Gly Gly Arg Ser Gln Ile	

	245	250	255	
tcc gtc aag tac cag ctg ctc tac gtg gcg gtt ccc agt ggc cct ccc				877
Ser Val Lys Tyr Gln Leu Leu Tyr Val Ala Val Pro Ser Gly Pro Pro				
	260	265	270	
tca aca acc atc ttg gct tct tca aac aaa gtg aaa agt ggg gac gac				925
Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Lys Ser Gly Asp Asp				
	275	280	285	
atc agt gtg ctc tgc act gtc ctg ggg gag ccc gat gtg gag gtg gag				973
Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu				
	290	295	300	
ttc acc tgg atc ttc cca ggg cag aag gat gaa agg cct gtg acg atc				1021
Phe Thr Trp Ile Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile				
	305	310	315	320
caa gac act tgg agg ttg atc cac aga gga ctg gga cac acc acg aga				1069
Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg				
	325	330	335	
atc tcc cag agt gtc att aca gtg gaa gac ttc gag acg att gat gca				1117
Ile Ser Gln Ser Val Ile Thr Val Glu Asp Phe Glu Thr Ile Asp Ala				
	340	345	350	
gga tat tac att tgc act gct cag aat ctt caa gga cag acc aca gta				1165
Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Gln Gly Gln Thr Thr Val				
	355	360	365	
gct acc act gtt gag ttt tcc tgacttgga aaggaaatgt aatgaactta				1216
Ala Thr Thr Val Glu Phe Ser				
	370	375		
tggaagccc atttgtgtac acagtcagct ttgggggttcc ttttattagt gctttgccag				1276
aggctgatgt caagcaccac accccaaccc cagcgtctcg tgagtcgcgac ccagacatcc				1336
aaactaaaag gaagtcaccc agtctattca cagaagtgtt aacttttcta acagaaagca				1396
tgattttgat tgcttaccta catacgtgtt cctagttttt atacatgtgt aaacaatttt				1456
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<210> 37
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 37

Met	Lys	Val	Trp	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	His	Glu	Ala	Leu
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Pro	Gly	Glu	Asn	Arg	Ile	Lys	Pro	Thr	Asn	Lys	Lys	Val	Lys	Pro	Lys	35	40	45
Ile	Pro	Lys	Met	Lys	Asp	Arg	Asp	Ser	Ala	Asn	Ser	Ala	Pro	Lys	Thr	50	55	60
Gln	Ser	Ile	Met	Met	Gln	Val	Leu	Asp	Lys	Gly	Arg	Phe	Gln	Lys	Pro	65	70	75
Ala	Ala	Thr	Leu	Ser	Leu	Leu	Ala	Gly	Gln	Thr	Val	Glu	Leu	Arg	Cys	85	90	95
Lys	Gly	Ser	Arg	Ile	Gly	Trp	Ser	Tyr	Pro	Ala	Tyr	Leu	Asp	Thr	Phe	100	105	110
Lys	Asp	Ser	Arg	Leu	Ser	Val	Lys	Gln	Asn	Glu	Arg	Tyr	Gly	Gln	Leu	115	120	125
Thr	Leu	Val	Asn	Ser	Thr	Ser	Ala	Asp	Thr	Gly	Glu	Phe	Ser	Cys	Trp	130	135	140
Val	Gln	Leu	Cys	Ser	Gly	Tyr	Ile	Cys	Arg	Lys	Asp	Glu	Ala	Lys	Thr	145	150	155
Gly	Ser	Thr	Tyr	Ile	Phe	Phe	Thr	Glu	Lys	Gly	Glu	Leu	Phe	Val	Pro	165	170	175
Ser	Pro	Ser	Tyr	Phe	Asp	Val	Val	Tyr	Leu	Asn	Pro	Asp	Arg	Gln	Ala	180	185	190
Val	Val	Pro	Cys	Arg	Val	Thr	Val	Leu	Ser	Ala	Lys	Val	Thr	Leu	His	195	200	205
Arg	Glu	Phe	Pro	Ala	Lys	Glu	Ile	Pro	Ala	Asn	Gly	Thr	Asp	Ile	Val	210	215	220
Tyr	Asp	Met	Lys	Arg	Gly	Phe	Val	Tyr	Leu	Gln	Pro	His	Ser	Glu	His	225	230	235
																240		

Gln Gly Val Val Tyr Cys Arg Ala Glu Ala Gly Gly Arg Ser Gln Ile
245 250 255

Ser Val Lys Tyr Gln Leu Leu Tyr Val Ala Val Pro Ser Gly Pro Pro
260 265 270

Ser Thr Thr Ile Leu Ala Ser Ser Asn Lys Val Lys Ser Gly Asp Asp
275 280 285

Ile Ser Val Leu Cys Thr Val Leu Gly Glu Pro Asp Val Glu Val Glu
290 295 300

Phe Thr Trp Ile Phe Pro Gly Gln Lys Asp Glu Arg Pro Val Thr Ile
305 310 315 320

Gln Asp Thr Trp Arg Leu Ile His Arg Gly Leu Gly His Thr Thr Arg
325 330 335

Ile Ser Gln Ser Val Ile Thr Val Glu Asp Phe Glu Thr Ile Asp Ala
340 345 350

Gly Tyr Tyr Ile Cys Thr Ala Gln Asn Leu Gln Gly Gln Thr Thr Val
355 360 365

Ala Thr Thr Val Glu Phe Ser
370 375

<210> 38
<211> 2379
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (69)..(2234)
<223> SF08, cDNA: NM_019696, Protein: NP_062670

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Met Trp Gly Leu Leu Leu Ala Val Thr Ala Phe Ala Pro Ser
1 5 10

gtc ggt ctg ggg ctg ggg gct ccc agc gcc tca gtg ccg ggc ctg gcg Val Gly Leu Gly Leu Gly Ala Pro Ser Ala Ser Val Pro Gly Leu Ala 15 20 25 30	158
ccg ggc tca acc ctg gct cca cac agc agc gtt gca cag ccg tcc aca Pro Gly Ser Thr Leu Ala Pro His Ser Ser Val Ala Gln Pro Ser Thr 35 40 45	206
aag gca aat gag acc tca gaa cgg cat gtc cgg ctt cga gtc atc aag Lys Ala Asn Glu Thr Ser Glu Arg His Val Arg Leu Arg Val Ile Lys 50 55 60	254
aaa aaa aag atc gtt gtc aag aag cga aag aag cta agg cac cct ggt Lys Lys Lys Ile Val Val Lys Lys Arg Lys Lys Leu Arg His Pro Gly 65 70 75	302
ccc ttg ggg act gct agg cct gtg gtg ccc act cac cca gca aag acc Pro Leu Gly Thr Ala Arg Pro Val Val Pro Thr His Pro Ala Lys Thr 80 85 90	350
ctc act ctc cct gag aaa caa gaa cca gga tgt ccc cct cta ggc ttg Leu Thr Leu Pro Glu Lys Gln Glu Pro Gly Cys Pro Pro Leu Gly Leu 95 100 105 110	398
gag tcc ttg agg gtt tca gat agc cag ctg gag gcc tcc agc agc cag Glu Ser Leu Arg Val Ser Asp Ser Gln Leu Glu Ala Ser Ser Ser Gln 115 120 125	446
tcc ttt ggt ctt gga gca cac cga gga cgg ctc aat atc cag tca ggt Ser Phe Gly Leu Gly Ala His Arg Gly Arg Leu Asn Ile Gln Ser Gly 130 135 140	494
ctg gag gac ggt gac ctg tat gat ggc gct tgg tgc gct gag caa caa Leu Glu Asp Gly Asp Leu Tyr Asp Gly Ala Trp Cys Ala Glu Gln Gln 145 150 155	542
gac act gaa cct tgg ctt cag gtg gat gca aag aat ccc gtc cgc ttc Asp Thr Glu Pro Trp Leu Gln Val Asp Ala Lys Asn Pro Val Arg Phe 160 165 170	590
gca gga att gtt aca cag ggc aga aac tct gtg tgg agg tat gac tgg Ala Gly Ile Val Thr Gln Gly Arg Asn Ser Val Trp Arg Tyr Asp Trp 175 180 185 190	638
gtc aca tca ttc aag gtc cag ttc agc aat gac agc cag acc tgg tgg Val Thr Ser Phe Lys Val Gln Phe Ser Asn Asp Ser Gln Thr Trp Trp 195 200 205	686
aag agt agg aac agt act gga atg gac ata gta ttt cct gcc aat tca Lys Ser Arg Asn Ser Thr Gly Met Asp Ile Val Phe Pro Ala Asn Ser 210 215 220	734
gac gca gag acc cca gtg ttg aac ctt ctg cca gag cct cag gtg gct Asp Ala Glu Thr Pro Val Leu Asn Leu Leu Pro Glu Pro Gln Val Ala	782

225						230						235						
cga	ttc	att	cgc	ctg	ctg	cct	cag	acc	tgg	ttt	cag	gga	ggt	gta	cct	830		
Arg	Phe	Ile	Arg	Leu	Leu	Pro	Gln	Thr	Trp	Phe	Gln	Gly	Gly	Val	Pro			
	240					245					250							
tgc	ctc	cgg	gca	gag	atc	ctg	gcc	tgc	cca	gtc	tca	gat	cct	aat	gac	878		
Cys	Leu	Arg	Ala	Glu	Ile	Leu	Ala	Cys	Pro	Val	Ser	Asp	Pro	Asn	Asp			
255					260					265					270			
ctg	ttc	cct	gag	gcc	cac	aca	ctg	gga	tct	tcg	aac	tct	ttg	gac	ttc	926		
Leu	Phe	Pro	Glu	Ala	His	Thr	Leu	Gly	Ser	Ser	Asn	Ser	Leu	Asp	Phe			
				275					280					285				
cgg	cat	cac	aat	tat	aaa	gct	atg	aga	aag	ctg	atg	aaa	cag	gtg	aat	974		
Arg	His	His	Asn	Tyr	Lys	Ala	Met	Arg	Lys	Leu	Met	Lys	Gln	Val	Asn			
			290					295					300					
gag	cag	tgc	ccc	aac	atc	acg	cgc	atc	tac	agc	atc	ggg	aag	agc	cac	1022		
Glu	Gln	Cys	Pro	Asn	Ile	Thr	Arg	Ile	Tyr	Ser	Ile	Gly	Lys	Ser	His			
		305					310					315						
cag	ggt	ttg	aag	ctg	tat	gtg	atg	gaa	atg	tca	gac	cat	cct	ggg	gag	1070		
Gln	Gly	Leu	Lys	Leu	Tyr	Val	Met	Glu	Met	Ser	Asp	His	Pro	Gly	Glu			
	320					325					330							
cat	gag	ctg	ggc	gag	ccc	gag	gtc	cgc	tac	gtg	gct	gga	atg	cat	ggg	1118		
His	Glu	Leu	Gly	Glu	Pro	Glu	Val	Arg	Tyr	Val	Ala	Gly	Met	His	Gly			
335					340					345					350			
aat	gag	gcc	ctg	ggg	cgg	gag	ttg	ctt	ctg	ctt	ttg	atg	cag	ttc	tta	1166		
Asn	Glu	Ala	Leu	Gly	Arg	Glu	Leu	Leu	Leu	Leu	Leu	Met	Gln	Phe	Leu			
				355				360						365				
tgc	cat	gag	ttc	ctg	cga	ggg	gac	ccg	cga	gtg	act	cgg	ctg	ctc	act	1214		
Cys	His	Glu	Phe	Leu	Arg	Gly	Asp	Pro	Arg	Val	Thr	Arg	Leu	Leu	Thr			
			370					375					380					
gag	aca	cga	atc	cat	cta	ttg	ccc	tcc	atg	aat	cct	gat	ggc	tat	gag	1262		
Glu	Thr	Arg	Ile	His	Leu	Leu	Pro	Ser	Met	Asn	Pro	Asp	Gly	Tyr	Glu			
		385					390					395						
act	gcc	tac	cac	agg	ggc	tca	gag	ctg	gtg	ggc	tgg	gca	gag	ggc	cgc	1310		
Thr	Ala	Tyr	His	Arg	Gly	Ser	Glu	Leu	Val	Gly	Trp	Ala	Glu	Gly	Arg			
	400					405					410							
tgg	acc	cac	cag	ggc	att	gac	ctt	aac	cac	aat	ttt	gct	gac	ctc	aac	1358		
Trp	Thr	His	Gln	Gly	Ile	Asp	Leu	Asn	His	Asn	Phe	Ala	Asp	Leu	Asn			
415					420					425					430			
aca	caa	ctg	tgg	tat	gca	gag	gat	gat	gga	ctg	gta	ccc	gac	act	gtc	1406		
Thr	Gln	Leu	Trp	Tyr	Ala	Glu	Asp	Asp	Gly	Leu	Val	Pro	Asp	Thr	Val			
				435				440					445					
ccc	aac	cat	cac	ctg	cca	ctg	cct	acc	tac	tat	aca	ttg	ccc	aat	gcc	1454		

Pro	Asn	His	His	Leu	Pro	Leu	Pro	Thr	Tyr	Tyr	Thr	Leu	Pro	Asn	Ala		
			450					455					460				
acc	gtg	gct	cct	gaa	acg	tgg	gca	gtg	atc	aaa	tgg	atg	aag	cgc	atc		1502
Thr	Val	Ala	Pro	Glu	Thr	Trp	Ala	Val	Ile	Lys	Trp	Met	Lys	Arg	Ile		
		465					470					475					
ccg	ttt	gtg	ctg	agt	gcc	aac	ctc	cat	ggg	ggc	gag	ctt	gtg	gtg	tcc		1550
Pro	Phe	Val	Leu	Ser	Ala	Asn	Leu	His	Gly	Gly	Glu	Leu	Val	Val	Ser		
	480					485					490						
tat	cct	ttc	gac	atg	act	cgg	act	ccg	tgg	gct	gct	cgt	gaa	ctc	act		1598
Tyr	Pro	Phe	Asp	Met	Thr	Arg	Thr	Pro	Trp	Ala	Ala	Arg	Glu	Leu	Thr		
495					500				505						510		
ccc	aca	cca	gat	gat	gct	gtc	ttc	cgc	tgg	ctc	agc	act	gtc	tat	gct		1646
Pro	Thr	Pro	Asp	Asp	Ala	Val	Phe	Arg	Trp	Leu	Ser	Thr	Val	Tyr	Ala		
				515					520					525			
ggc	acg	aat	agg	gcc	atg	cag	gat	acc	gac	cgc	cga	cct	tgt	cat	agc		1694
Gly	Thr	Asn	Arg	Ala	Met	Gln	Asp	Thr	Asp	Arg	Arg	Pro	Cys	His	Ser		
			530					535					540				
cag	gac	ttc	tcc	ttg	cat	ggc	aac	gtc	atc	aat	gga	gcc	gac	tgg	cac		1742
Gln	Asp	Phe	Ser	Leu	His	Gly	Asn	Val	Ile	Asn	Gly	Ala	Asp	Trp	His		
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aca	gtt	cct	ggg	agc	atg	aac	gac	ttc	agc	tac	cta	cac	acc	aat	tgc		1790
Thr	Val	Pro	Gly	Ser	Met	Asn	Asp	Phe	Ser	Tyr	Leu	His	Thr	Asn	Cys		
	560					565					570						
ttt	gag	gtc	aca	gtg	gag	ctg	tcc	tgt	gac	aag	ttc	cct	cat	gag	aag		1838
Phe	Glu	Val	Thr	Val	Glu	Leu	Ser	Cys	Asp	Lys	Phe	Pro	His	Glu	Lys		
575					580				585						590		
gag	ctg	cct	cag	gag	tgg	gaa	aac	aac	aaa	gat	gct	ctt	ctc	acc	tac		1886
Glu	Leu	Pro	Gln	Glu	Trp	Glu	Asn	Asn	Lys	Asp	Ala	Leu	Leu	Thr	Tyr		
				595					600					605			
ctg	gag	cag	gtg	cgc	atg	ggc	att	act	gga	gtt	gtc	cgg	gat	aaa	gac		1934
Leu	Glu	Gln	Val	Arg	Met	Gly	Ile	Thr	Gly	Val	Val	Arg	Asp	Lys	Asp		
			610					615					620				
aca	gag	ctc	ggc	att	gcg	gat	gct	gtc	att	gcc	gtg	gag	ggc	att	aac		1982
Thr	Glu	Leu	Gly	Ile	Ala	Asp	Ala	Val	Ile	Ala	Val	Glu	Gly	Ile	Asn		
		625					630					635					
cac	gat	gtt	aca	aca	gct	tgg	ggc	gga	gat	tac	tgg	cgg	ctg	ctg	aca		2030
His	Asp	Val	Thr	Thr	Ala	Trp	Gly	Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Thr		
	640					645					650						
cct	ggg	gac	tat	gtg	gtg	aca	gcc	agt	gct	gag	ggg	tac	cat	aca	gtc		2078
Pro	Gly	Asp	Tyr	Val	Val	Thr	Ala	Ser	Ala	Glu	Gly	Tyr	His	Thr	Val		
655					660					665					670		

aga caa cac tgt cag gtc acc ttt gaa gag ggc cct gtt ccc tgc aat	2126
Arg Gln His Cys Gln Val Thr Phe Glu Glu Gly Pro Val Pro Cys Asn	
675 680 685	
ttc cta ctc acc aag act ccc aaa gag agg ctt cga gaa ctg ttg gca	2174
Phe Leu Leu Thr Lys Thr Pro Lys Glu Arg Leu Arg Glu Leu Leu Ala	
690 695 700	
aca cga ggg aag ttg ccc cca gac ctt cgg agg aag ctg gag cgg ctg	2222
Thr Arg Gly Lys Leu Pro Pro Asp Leu Arg Arg Lys Leu Glu Arg Leu	
705 710 715	
agg gga cag aag taacgtcttc agctgaagag agccacatcc ttggacaggc	2274
Arg Gly Gln Lys	
720	
tggacctgtc cagaactgaa ggaggagggg gaagagagag ggacggggta gaagaggtgc	2334
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35 40 45	
Asn Glu Thr Ser Glu Arg His Val Arg Leu Arg Val Ile Lys Lys Lys	
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Lys Ile Val Val Lys Lys Arg Lys Lys Leu Arg His Pro Gly Pro Leu	
65 70 75 80	
Gly Thr Ala Arg Pro Val Val Pro Thr His Pro Ala Lys Thr Leu Thr	
85 90 95	
Leu Pro Glu Lys Gln Glu Pro Gly Cys Pro Pro Leu Gly Leu Glu Ser	
100 105 110	

Leu Arg Val Ser Asp Ser Gln Leu Glu Ala Ser Ser Ser Gln Ser Phe
 115 120 125

Gly Leu Gly Ala His Arg Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu
 130 135 140

Asp Gly Asp Leu Tyr Asp Gly Ala Trp Cys Ala Glu Gln Gln Asp Thr
 145 150 155 160

Glu Pro Trp Leu Gln Val Asp Ala Lys Asn Pro Val Arg Phe Ala Gly
 165 170 175

Ile Val Thr Gln Gly Arg Asn Ser Val Trp Arg Tyr Asp Trp Val Thr
 180 185 190

Ser Phe Lys Val Gln Phe Ser Asn Asp Ser Gln Thr Trp Trp Lys Ser
 195 200 205

Arg Asn Ser Thr Gly Met Asp Ile Val Phe Pro Ala Asn Ser Asp Ala
 210 215 220

Glu Thr Pro Val Leu Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe
 225 230 235 240

Ile Arg Leu Leu Pro Gln Thr Trp Phe Gln Gly Gly Val Pro Cys Leu
 245 250 255

Arg Ala Glu Ile Leu Ala Cys Pro Val Ser Asp Pro Asn Asp Leu Phe
 260 265 270

Pro Glu Ala His Thr Leu Gly Ser Ser Asn Ser Leu Asp Phe Arg His
 275 280 285

His Asn Tyr Lys Ala Met Arg Lys Leu Met Lys Gln Val Asn Glu Gln
 290 295 300

Cys Pro Asn Ile Thr Arg Ile Tyr Ser Ile Gly Lys Ser His Gln Gly
 305 310 315 320

Leu Lys Leu Tyr Val Met Glu Met Ser Asp His Pro Gly Glu His Glu
 325 330 335

Leu Gly Glu Pro Glu Val Arg Tyr Val Ala Gly Met His Gly Asn Glu
340 345 350

Ala Leu Gly Arg Glu Leu Leu Leu Leu Met Gln Phe Leu Cys His
355 360 365

Glu Phe Leu Arg Gly Asp Pro Arg Val Thr Arg Leu Leu Thr Glu Thr
370 375 380

Arg Ile His Leu Leu Pro Ser Met Asn Pro Asp Gly Tyr Glu Thr Ala
385 390 395 400

Tyr His Arg Gly Ser Glu Leu Val Gly Trp Ala Glu Gly Arg Trp Thr
405 410 415

His Gln Gly Ile Asp Leu Asn His Asn Phe Ala Asp Leu Asn Thr Gln
420 425 430

Leu Trp Tyr Ala Glu Asp Asp Gly Leu Val Pro Asp Thr Val Pro Asn
435 440 445

His His Leu Pro Leu Pro Thr Tyr Tyr Thr Leu Pro Asn Ala Thr Val
450 455 460

Ala Pro Glu Thr Trp Ala Val Ile Lys Trp Met Lys Arg Ile Pro Phe
465 470 475 480

Val Leu Ser Ala Asn Leu His Gly Gly Glu Leu Val Val Ser Tyr Pro
485 490 495

Phe Asp Met Thr Arg Thr Pro Trp Ala Ala Arg Glu Leu Thr Pro Thr
500 505 510

Pro Asp Asp Ala Val Phe Arg Trp Leu Ser Thr Val Tyr Ala Gly Thr
515 520 525

Asn Arg Ala Met Gln Asp Thr Asp Arg Arg Pro Cys His Ser Gln Asp
530 535 540

Phe Ser Leu His Gly Asn Val Ile Asn Gly Ala Asp Trp His Thr Val

545		550		555		560
Pro Gly Ser Met	Asn Asp Phe Ser Tyr	Leu His Thr Asn Cys	Phe Glu			
	565	570	575			
Val Thr Val	Glu Leu Ser Cys Asp	Lys Phe Pro His Glu	Lys Glu Leu			
	580	585	590			
Pro Gln Glu Trp	Glu Asn Asn Lys Asp	Ala Leu Leu Thr	Tyr Leu Glu			
	595	600	605			
Gln Val Arg Met	Gly Ile Thr Gly Val	Val Arg Asp Lys	Asp Thr Glu			
	610	615	620			
Leu Gly Ile Ala	Asp Ala Val Ile Ala	Val Glu Gly Ile	Asn His Asp			
	625	630	635			640
Val Thr Thr Ala	Trp Gly Gly Asp Tyr	Trp Arg Leu Leu	Thr Pro Gly			
	645	650	655			
Asp Tyr Val Val	Thr Ala Ser Ala	Glu Gly Tyr His	Thr Val Arg Gln			
	660	665	670			
His Cys Gln Val	Thr Phe Glu Glu	Gly Pro Val Pro	Cys Asn Phe Leu			
	675	680	685			
Leu Thr Lys Thr	Pro Lys Glu Arg	Leu Arg Glu Leu	Leu Ala Thr Arg			
	690	695	700			
Gly Lys Leu Pro	Pro Asp Leu Arg	Arg Lys Leu Glu	Arg Leu Arg Gly			
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Gln Lys

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<222> (65)..(2266)

<223> SF08, cDNA: NM_019609, Protein: NP_062555

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Met Trp Gly Leu Leu Leu Ala Leu Ala Ala Phe Ala Pro Ala Val	
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ggc ccg gct ctg ggg gcg ccc agg aac tcg gtg ctg ggc ctc gcg cag	157
Gly Pro Ala Leu Gly Ala Pro Arg Asn Ser Val Leu Gly Leu Ala Gln	
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ccc ggg acc acc aag gtc cca ggc tcg acc ccg gcc ctg cat agc agc	205
Pro Gly Thr Thr Lys Val Pro Gly Ser Thr Pro Ala Leu His Ser Ser	
35 40 45	
ccg gca cag ccg ccg gcg gag aca gct aac ggg acc tca gaa cag cat	253
Pro Ala Gln Pro Pro Ala Glu Thr Ala Asn Gly Thr Ser Glu Gln His	
50 55 60	
gtc cgg att cga gtc atc aag aag aaa aag gtc att atg aag aag cgg	301
Val Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg	
65 70 75	
aag aag cta act cta act cgc ccc acc cca ctg gtg act gcc ggg ccc	349
Lys Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro	
80 85 90 95	
ctt gtg acc ccc act cca gca ggg acc ctc gac ccc gct gag aaa caa	397
Leu Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln	
100 105 110	
gaa aca ggc tgt cct cct ttg ggt ctg gag tcc ctg cga gtt tca gat	445
Glu Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp	
115 120 125	
agc cgg ctt gag gca tcc agc agc cag tcc ttt ggt ctt gga cca cac	493
Ser Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His	
130 135 140	
cga gga cgg ctc aac att cag tca ggc ctg gag gac ggc gat cta tat	541
Arg Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr	
145 150 155	
gat gga gcc tgg tgt gct gag gag cag gac gcc gat cca tgg ttt cag	589
Asp Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln	
160 165 170 175	
gtg gac gct ggg cac ccc acc cgc ttc tcg ggt gtt atc aca cag ggc	637
Val Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly	
180 185 190	
agg aac tct gtc tgg agg tat gac tgg gtc aca tca tac aag gtc cag	685

Arg	Asn	Ser	Val	Trp	Arg	Tyr	Asp	Trp	Val	Thr	Ser	Tyr	Lys	Val	Gln	
			195					200					205			
ttc	agc	aat	gac	agt	cgg	acc	tgg	tgg	gga	agt	agg	aac	cac	agc	agt	733
Phe	Ser	Asn	Asp	Ser	Arg	Thr	Trp	Trp	Gly	Ser	Arg	Asn	His	Ser	Ser	
		210					215					220				
ggg	atg	gac	gca	gta	ttt	cct	gcc	aat	tca	gac	cca	gaa	act	cca	gtg	781
Gly	Met	Asp	Ala	Val	Phe	Pro	Ala	Asn	Ser	Asp	Pro	Glu	Thr	Pro	Val	
	225					230					235					
ctg	aac	ctc	ctg	ccg	gag	ccc	cag	gtg	gcc	cgc	ttc	att	cgc	ctg	ctg	829
Leu	Asn	Leu	Leu	Pro	Glu	Pro	Gln	Val	Ala	Arg	Phe	Ile	Arg	Leu	Leu	
240					245					250					255	
ccc	cag	acc	tgg	ctc	cag	gga	ggc	gcg	cct	tgc	ctc	cgg	gca	gag	atc	877
Pro	Gln	Thr	Trp	Leu	Gln	Gly	Gly	Ala	Pro	Cys	Leu	Arg	Ala	Glu	Ile	
				260					265					270		
ctg	gcc	tgc	cca	gtc	tca	gac	ccc	aat	gac	cta	ttc	ctt	gag	gcc	cct	925
Leu	Ala	Cys	Pro	Val	Ser	Asp	Pro	Asn	Asp	Leu	Phe	Leu	Glu	Ala	Pro	
			275					280					285			
gcg	tcg	gga	tcc	tct	gac	cct	cta	gac	ttt	cag	cat	cac	aat	tac	aag	973
Ala	Ser	Gly	Ser	Ser	Asp	Pro	Leu	Asp	Phe	Gln	His	His	Asn	Tyr	Lys	
		290					295					300				
gcc	atg	agg	aag	ctg	atg	aag	cag	gta	caa	gag	caa	tgc	ccc	aac	atc	1021
Ala	Met	Arg	Lys	Leu	Met	Lys	Gln	Val	Gln	Glu	Gln	Cys	Pro	Asn	Ile	
	305					310					315					
acc	cgc	atc	tac	agc	att	ggg	aag	agc	tac	cag	ggc	ctg	aag	ctg	tat	1069
Thr	Arg	Ile	Tyr	Ser	Ile	Gly	Lys	Ser	Tyr	Gln	Gly	Leu	Lys	Leu	Tyr	
320					325					330					335	
gtg	atg	gaa	atg	tcg	gac	aag	cct	ggg	gag	cat	gag	ctg	ggg	gag	cct	1117
Val	Met	Glu	Met	Ser	Asp	Lys	Pro	Gly	Glu	His	Glu	Leu	Gly	Glu	Pro	
				340				345					350			
gag	gtg	cgc	tac	gtg	gct	ggc	atg	cat	ggg	aac	gag	gcc	ctg	ggg	cgg	1165
Glu	Val	Arg	Tyr	Val	Ala	Gly	Met	His	Gly	Asn	Glu	Ala	Leu	Gly	Arg	
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gag	ttg	ctt	ctg	ctc	ctg	atg	cag	ttc	ctg	tgc	cat	gag	ttc	ctg	cga	1213
Glu	Leu	Leu	Leu	Leu	Leu	Met	Gln	Phe	Leu	Cys	His	Glu	Phe	Leu	Arg	
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Gly	Asn	Pro	Arg	Val	Thr	Arg	Leu	Leu	Ser	Glu	Met	Arg	Ile	His	Leu	
	385					390					395					
ctg	ccc	tcc	atg	aac	cct	gat	ggc	tat	gag	atc	gcc	tac	cac	cgg	ggc	1309
Leu	Pro	Ser	Met	Asn	Pro	Asp	Gly	Tyr	Glu	Ile	Ala	Tyr	His	Arg	Gly	
400					405					410					415	

tca gag ctg gtg ggc tgg gcc gag ggc cgc tgg aac aac cag agc atc	1357
Ser Glu Leu Val Gly Trp Ala Glu Gly Arg Trp Asn Asn Gln Ser Ile	
420 425 430	
gat ctt aac cat aat ttt gct gac ctc aac aca cca ctg tgg gaa gca	1405
Asp Leu Asn His Asn Phe Ala Asp Leu Asn Thr Pro Leu Trp Glu Ala	
435 440 445	
cag gac gat ggg aag gtg ccc cac atc gtc ccc aac cat cac ctg cca	1453
Gln Asp Asp Gly Lys Val Pro His Ile Val Pro Asn His His Leu Pro	
450 455 460	
ttg ccc act tac tac acc ctg ccc aat gcc acc gtg gct cct gaa acg	1501
Leu Pro Thr Tyr Tyr Thr Leu Pro Asn Ala Thr Val Ala Pro Glu Thr	
465 470 475	
cgg gca gta atc aag tgg atg aag cgg atc ccc ttt gtg cta agt gcc	1549
Arg Ala Val Ile Lys Trp Met Lys Arg Ile Pro Phe Val Leu Ser Ala	
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aac ctc cac ggg ggt gag ctc gtg gtg tcc tac cca ttc gac atg act	1597
Asn Leu His Gly Gly Glu Leu Val Val Ser Tyr Pro Phe Asp Met Thr	
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Arg Thr Pro Trp Ala Ala Arg Glu Leu Thr Pro Thr Pro Asp Asp Ala	
515 520 525	
gtg ttt cgc tgg ctc agc act gtc tat gct ggc agt aat ctg gcc atg	1693
Val Phe Arg Trp Leu Ser Thr Val Tyr Ala Gly Ser Asn Leu Ala Met	
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Gln Asp Thr Ser Arg Arg Pro Cys His Ser Gln Asp Phe Ser Val His	
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Gly Asn Ile Ile Asn Gly Ala Asp Trp His Thr Val Pro Gly Ser Met	
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Asn Asp Phe Ser Tyr Leu His Thr Asn Cys Phe Glu Val Thr Val Glu	
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Leu Ser Cys Asp Lys Phe Pro His Glu Asn Glu Leu Pro Gln Glu Trp	
595 600 605	
gag aac aac aaa gac gcc ctc ctc acc tac ctg gag cag gtg cgc atg	1933
Glu Asn Asn Lys Asp Ala Leu Leu Thr Tyr Leu Glu Gln Val Arg Met	
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ggc att gca gga gtg gtg agg gac aag gac acg gag ctt ggg att gct	1981
Gly Ile Ala Gly Val Val Arg Asp Lys Asp Thr Glu Leu Gly Ile Ala	
625 630 635	

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Asp Ala Val Ile Ala Val Asp Gly Ile Asn His Asp Val Thr Thr Ala	
640 645 650 655	
tgg ggc ggg gat tat tgg cgt ctg ctg acc cca ggg gac tac atg gtg	2077
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Thr Ala Ser Ala Glu Gly Tyr His Ser Val Thr Arg Asn Cys Arg Val	
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acc ttt gaa gag ggc ccc ttc ccc tgc aat ttc gtg ctc acc aag act	2173
Thr Phe Glu Glu Gly Pro Phe Pro Cys Asn Phe Val Leu Thr Lys Thr	
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ccc aaa cag agg ctg cgc gag ctg ctg gca gct ggg gcc aag gtg ccc	2221
Pro Lys Gln Arg Leu Arg Glu Leu Leu Ala Ala Gly Ala Lys Val Pro	
705 710 715	
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Pro Asp Leu Arg Arg Arg Leu Glu Arg Leu Arg Gly Gln Lys Asp	
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35 40 45

Ala Gln Pro Pro Ala Glu Thr Ala Asn Gly Thr Ser Glu Gln His Val
50 55 60

Arg	Ile	Arg	Val	Ile	Lys	Lys	Lys	Lys	Val	Ile	Met	Lys	Lys	Arg	Lys	65	70	75	80
Lys	Leu	Thr	Leu	Thr	Arg	Pro	Thr	Pro	Leu	Val	Thr	Ala	Gly	Pro	Leu	85	90	95	
Val	Thr	Pro	Thr	Pro	Ala	Gly	Thr	Leu	Asp	Pro	Ala	Glu	Lys	Gln	Glu	100	105	110	
Thr	Gly	Cys	Pro	Pro	Leu	Gly	Leu	Glu	Ser	Leu	Arg	Val	Ser	Asp	Ser	115	120	125	
Arg	Leu	Glu	Ala	Ser	Ser	Ser	Gln	Ser	Phe	Gly	Leu	Gly	Pro	His	Arg	130	135	140	
Gly	Arg	Leu	Asn	Ile	Gln	Ser	Gly	Leu	Glu	Asp	Gly	Asp	Leu	Tyr	Asp	145	150	155	160
Gly	Ala	Trp	Cys	Ala	Glu	Glu	Gln	Asp	Ala	Asp	Pro	Trp	Phe	Gln	Val	165	170	175	
Asp	Ala	Gly	His	Pro	Thr	Arg	Phe	Ser	Gly	Val	Ile	Thr	Gln	Gly	Arg	180	185	190	
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Ser	Asn	Asp	Ser	Arg	Thr	Trp	Trp	Gly	Ser	Arg	Asn	His	Ser	Ser	Gly	210	215	220	
Met	Asp	Ala	Val	Phe	Pro	Ala	Asn	Ser	Asp	Pro	Glu	Thr	Pro	Val	Leu	225	230	235	240
Asn	Leu	Leu	Pro	Glu	Pro	Gln	Val	Ala	Arg	Phe	Ile	Arg	Leu	Leu	Pro	245	250	255	
Gln	Thr	Trp	Leu	Gln	Gly	Gly	Ala	Pro	Cys	Leu	Arg	Ala	Glu	Ile	Leu	260	265	270	
Ala	Cys	Pro	Val	Ser	Asp	Pro	Asn	Asp	Leu	Phe	Leu	Glu	Ala	Pro	Ala	275	280	285	

Ser Gly Ser Ser Asp Pro Leu Asp Phe Gln His His Asn Tyr Lys Ala
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Met Arg Lys Leu Met Lys Gln Val Gln Glu Gln Cys Pro Asn Ile Thr
 305 310 315 320

Arg Ile Tyr Ser Ile Gly Lys Ser Tyr Gln Gly Leu Lys Leu Tyr Val
 325 330 335

Met Glu Met Ser Asp Lys Pro Gly Glu His Glu Leu Gly Glu Pro Glu
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Val Arg Tyr Val Ala Gly Met His Gly Asn Glu Ala Leu Gly Arg Glu
 355 360 365

Leu Leu Leu Leu Leu Met Gln Phe Leu Cys His Glu Phe Leu Arg Gly
 370 375 380

Asn Pro Arg Val Thr Arg Leu Leu Ser Glu Met Arg Ile His Leu Leu
 385 390 395 400

Pro Ser Met Asn Pro Asp Gly Tyr Glu Ile Ala Tyr His Arg Gly Ser
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Glu Leu Val Gly Trp Ala Glu Gly Arg Trp Asn Asn Gln Ser Ile Asp
 420 425 430

Leu Asn His Asn Phe Ala Asp Leu Asn Thr Pro Leu Trp Glu Ala Gln
 435 440 445

Asp Asp Gly Lys Val Pro His Ile Val Pro Asn His His Leu Pro Leu
 450 455 460

Pro Thr Tyr Tyr Thr Leu Pro Asn Ala Thr Val Ala Pro Glu Thr Arg
 465 470 475 480

Ala Val Ile Lys Trp Met Lys Arg Ile Pro Phe Val Leu Ser Ala Asn
 485 490 495

Leu His Gly Gly Glu Leu Val Val Ser Tyr Pro Phe Asp Met Thr Arg
 500 505 510

Thr	Pro	Trp	Ala	Ala	Arg	Glu	Leu	Thr	Pro	Thr	Pro	Asp	Asp	Ala	Val
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Phe	Arg	Trp	Leu	Ser	Thr	Val	Tyr	Ala	Gly	Ser	Asn	Leu	Ala	Met	Gln
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Asp	Thr	Ser	Arg	Arg	Pro	Cys	His	Ser	Gln	Asp	Phe	Ser	Val	His	Gly
545					550					555					560
Asn	Ile	Ile	Asn	Gly	Ala	Asp	Trp	His	Thr	Val	Pro	Gly	Ser	Met	Asn
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Asp	Phe	Ser	Tyr	Leu	His	Thr	Asn	Cys	Phe	Glu	Val	Thr	Val	Glu	Leu
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Ser	Cys	Asp	Lys	Phe	Pro	His	Glu	Asn	Glu	Leu	Pro	Gln	Glu	Trp	Glu
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Asn	Asn	Lys	Asp	Ala	Leu	Leu	Thr	Tyr	Leu	Glu	Gln	Val	Arg	Met	Gly
	610					615					620				
Ile	Ala	Gly	Val	Val	Arg	Asp	Lys	Asp	Thr	Glu	Leu	Gly	Ile	Ala	Asp
625					630					635					640
Ala	Val	Ile	Ala	Val	Asp	Gly	Ile	Asn	His	Asp	Val	Thr	Thr	Ala	Trp
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Gly	Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Thr	Pro	Gly	Asp	Tyr	Met	Val	Thr
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Ala	Ser	Ala	Glu	Gly	Tyr	His	Ser	Val	Thr	Arg	Asn	Cys	Arg	Val	Thr
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Phe	Glu	Glu	Gly	Pro	Phe	Pro	Cys	Asn	Phe	Val	Leu	Thr	Lys	Thr	Pro
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<223>   SF09, cDNA: NM 139295, Protein: NP 647456
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 <213> Mus musculus

<400> 43

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Glu Met Ser Pro Gln Glu Leu Gln Leu His Tyr Phe Lys Met His Asp	65	70	75
Tyr Asp Gly Asn Ser Leu Leu Asp Gly Leu Glu Leu Ser Ile Ala Ile	85	90	95
Thr His Val His Lys Glu Glu Gly Ser Glu Gln Ala Pro Val Met Ser	100	105	110
Glu Asp Glu Leu Val Ser Ile Ile Asp Gly Val Leu Arg Asp Asp Asp	115	120	125
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 <212> PRT
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<400> 45

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 35 40 45

Gln Glu His Ile Met Glu His Leu Glu Gly Val Ile Asn Lys Pro Glu
 50 55 60

Ala Glu Met Ser Pro Gln Glu Leu Gln Leu His Tyr Phe Lys Met His
 65 70 75 80

Asp Tyr Asp Gly Asn Asn Leu Leu Asp Gly Leu Glu Leu Ser Thr Ala
 85 90 95

Ile Thr His Val His Lys Glu Glu Gly Ser Glu Gln Ala Pro Leu Met
 100 105 110

Ser Glu Asp Glu Leu Ile Asn Ile Ile Asp Gly Val Leu Arg Asp Asp
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Asp Lys Asn Asn Asp Gly Tyr Ile Asp Tyr Ala Glu Phe Ala Lys Ser
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Leu Gln
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 <212> DNA
 <213> Mus musculus

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 <223> SF10, cDNA: NM_029568, Protein: NP_083844

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 <212> PRT
 <213> Mus musculus

<400> 47

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 <223> SF10, cDNA: NM_002404, Protein: NP_002395

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10 15 20 25		
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Arg Gly Asp Ala Leu Glu Arg Phe Cys Leu Gln Gln Pro Leu Asp Cys		
	30 35 40	
gac gac atc tat gcc cag ggc tac cag tca gac ggc gtg tac ctc atc		196
Asp Asp Ile Tyr Ala Gln Gly Tyr Gln Ser Asp Gly Val Tyr Leu Ile		
	45 50 55	
tac ccc tcg ggc ccc agt gtg cct gtg ccc gtc ttc tgt gac atg acc		244
Tyr Pro Ser Gly Pro Ser Val Pro Val Pro Val Phe Cys Asp Met Thr		
	60 65 70	
acc gag ggc ggg aag tgg acg gtt ttc cag aag aga ttc aat ggc tca		292
Thr Glu Gly Gly Lys Trp Thr Val Phe Gln Lys Arg Phe Asn Gly Ser		
	75 80 85	
gta agt ttc ttc cgc ggc tgg aat gac tac aag ctg ggc ttc ggc cgt		340
Val Ser Phe Phe Arg Gly Trp Asn Asp Tyr Lys Leu Gly Phe Gly Arg		
	90 95 100 105	
gct gat gga gag tac tgg ctg ggg ctg cag aac atg cac ctc ctg aca		388
Ala Asp Gly Glu Tyr Trp Leu Gly Leu Gln Asn Met His Leu Leu Thr		
	110 115 120	
ctg aag cag aag tat gag ctg cga gtg gac ttg gag gac ttt gag aac		436
Leu Lys Gln Lys Tyr Glu Leu Arg Val Asp Leu Glu Asp Phe Glu Asn		
	125 130 135	
aac acg gcc tat gcc aag tac gct gac ttc tcc atc tcc ccg aac gcg		484
Asn Thr Ala Tyr Ala Lys Tyr Ala Asp Phe Ser Ile Ser Pro Asn Ala		
	140 145 150	
gtc agc gca gag gag gat ggc tac acc ctc ttt gtg gca ggc ttt gag		532
Val Ser Ala Glu Glu Asp Gly Tyr Thr Leu Phe Val Ala Gly Phe Glu		

155	160	165	
gat ggc ggg gca ggt gac tcc ctg tcc tac cac agt ggc cag aag ttc			580
Asp Gly Gly Ala Gly Asp Ser Leu Ser Tyr His Ser Gly Gln Lys Phe			
170	175	180	185
tct acc ttc gac cgg gac cag gac ctc ttt gtg cag aac tgc gca gct			628
Ser Thr Phe Asp Arg Asp Gln Asp Leu Phe Val Gln Asn Cys Ala Ala			
	190	195	200
ctc tcc tca gga gcc ttc tgg ttc cgc agc tgc cac ttt gcc aac ctc			676
Leu Ser Ser Gly Ala Phe Trp Phe Arg Ser Cys His Phe Ala Asn Leu			
	205	210	215
aat ggc ttc tac cta ggt ggc tcc cac ctc tct tat gcc aat ggc atc			724
Asn Gly Phe Tyr Leu Gly Gly Ser His Leu Ser Tyr Ala Asn Gly Ile			
	220	225	230
aac tgg gcc cag tgg aag ggc ttc tac tac tcc ctc aaa cgc act gag			772
Asn Trp Ala Gln Trp Lys Gly Phe Tyr Tyr Ser Leu Lys Arg Thr Glu			
	235	240	245
atg aaa atc cgc cgg gcc tgaagggctg gccccctcag gcacctttcc			820
Met Lys Ile Arg Arg Ala			
250	255		
tccccctggac acccatgggc tccatgagtg ctccctctgc tgccccctgat gcatgcttct			880
gctgattccc gagcaccaac tccttacaag ggggccttgt ggctctcagc catgccacat			940
ccctgtcaca caccaggggc atccattcct aagccagacc cggctcccct acacctgaag			1000
ttacactgcc agcagttccc caggcctctt ccgagaggca catggttcta gcctggacct			1060
ggctgggctc catgagaatg agttgcctcc accctgtccc aacagctgac agccaggagc			1120
cactctccca gctgcaggcc tttgtggtcc atcttgtcct gcttctcac tgtggacccc			1180
tgtctgggcc accctagtgt gctaagctga gcagtgcagt gtgaacaggg cccatgggtgt			1240
attctaggcc acagcccagc actcctctgg gctgctctca aaccatgtcc catcttcagc			1300
atccctccca ccaacttact cccctgtggt gagtaccgtg gaaccccagc ccacctcact			1360
atcatactca gcttcccctg atggcccatc ccagcccctg aagctctatg ccaagaacac			1420
agctaccgca caccaccctg aaacagccac agccaaggta ggcatagcata tgagggtcttc			1480
cccataccct ctgggtgttg agaggtttag ccacatgagg gagcagagga caatctctgc			1540
agggtggga gtgggtaggg actgaaggct tcaataaacc ttcagaacct gaatgaactg			1600
gcttcataca cacaacata tttgtttatc ccccaaattgt aggcacctgg ctctccttg			1660
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aagggaacct tgtattttcac aggcctcatt ttgatggcaa aaagacagtg taataataac 1780
 ataataataa taaaaatata atactgaaaa ggaaaaaaaaa aaaaaaaaaa 1830

<210> 49
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 49

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Phe Cys Leu Gln Gln Pro Leu Asp Cys Asp Asp Ile Tyr Ala Gln Gly
 35 40 45

Tyr Gln Ser Asp Gly Val Tyr Leu Ile Tyr Pro Ser Gly Pro Ser Val
 50 55 60

Pro Val Pro Val Phe Cys Asp Met Thr Thr Glu Gly Gly Lys Trp Thr
 65 70 75 80

Val Phe Gln Lys Arg Phe Asn Gly Ser Val Ser Phe Phe Arg Gly Trp
 85 90 95

Asn Asp Tyr Lys Leu Gly Phe Gly Arg Ala Asp Gly Glu Tyr Trp Leu
 100 105 110

Gly Leu Gln Asn Met His Leu Leu Thr Leu Lys Gln Lys Tyr Glu Leu
 115 120 125

Arg Val Asp Leu Glu Asp Phe Glu Asn Asn Thr Ala Tyr Ala Lys Tyr
 130 135 140

Ala Asp Phe Ser Ile Ser Pro Asn Ala Val Ser Ala Glu Glu Asp Gly
 145 150 155 160

Tyr Thr Leu Phe Val Ala Gly Phe Glu Asp Gly Gly Ala Gly Asp Ser
 165 170 175

Leu Ser Tyr His Ser Gly Gln Lys Phe Ser Thr Phe Asp Arg Asp Gln
180 185 190

Asp Leu Phe Val Gln Asn Cys Ala Ala Leu Ser Ser Gly Ala Phe Trp
195 200 205

Phe Arg Ser Cys His Phe Ala Asn Leu Asn Gly Phe Tyr Leu Gly Gly
210 215 220

Ser His Leu Ser Tyr Ala Asn Gly Ile Asn Trp Ala Gln Trp Lys Gly
225 230 235 240

Phe Tyr Tyr Ser Leu Lys Arg Thr Glu Met Lys Ile Arg Arg Ala
245 250 255

<210> 50
<211> 749
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (93)..(512)
<223> SF11, cDNA: NM_009976, Protein: NP_034106

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gttgagagctt tatccctttg tcctagccaa cc atg gcc agc ccg ctg cgc tcc 113
Met Ala Ser Pro Leu Arg Ser
1 5
ttg ctg ttc ctg ctg gcc gtc ctg gcc gtg gcc tgg gcg gcg acc cca 161
Leu Leu Phe Leu Leu Ala Val Leu Ala Val Ala Trp Ala Ala Thr Pro
10 15 20
aaa caa ggc ccg cga atg ttg gga gcc ccg gag gag gca gat gcc aat 209
Lys Gln Gly Pro Arg Met Leu Gly Ala Pro Glu Glu Ala Asp Ala Asn
25 30 35
gag gaa ggc gtg cgg cga gcg ttg gac ttc gct gtg agc gag tac aac 257
Glu Glu Gly Val Arg Arg Ala Leu Asp Phe Ala Val Ser Glu Tyr Asn
40 45 50 55
aag ggc agc aac gat gcg tac cac agc cgc gcc ata cag gtg gtg aga 305
Lys Gly Ser Asn Asp Ala Tyr His Ser Arg Ala Ile Gln Val Val Arg
60 65 70

gct	cgt	aag	cag	ctc	gtg	gct	gga	gtg	aac	tat	ttt	ttg	gat	gtg	gag	353
Ala	Arg	Lys	Gln	Leu	Val	Ala	Gly	Val	Asn	Tyr	Phe	Leu	Asp	Val	Glu	
			75					80					85			

atg	ggc	cga	act	aca	tgt	acc	aag	tcc	cag	aca	aat	ttg	act	gac	tgt	401
Met	Gly	Arg	Thr	Thr	Cys	Thr	Lys	Ser	Gln	Thr	Asn	Leu	Thr	Asp	Cys	
		90					95					100				

cct	ttc	cat	gac	cag	ccc	cat	ctg	atg	agg	aag	gca	ctc	tgc	tcc	ttc	449
Pro	Phe	His	Asp	Gln	Pro	His	Leu	Met	Arg	Lys	Ala	Leu	Cys	Ser	Phe	
	105					110					115					

cag	atc	tac	agc	gtg	ccc	tgg	aaa	ggc	aca	cac	tcc	ctg	aca	aaa	ttc	497
Gln	Ile	Tyr	Ser	Val	Pro	Trp	Lys	Gly	Thr	His	Ser	Leu	Thr	Lys	Phe	
120					125				130					135		

agc	tgc	aaa	aat	gcc	taagggctga	gtctagaagg	atcatgcaga	ctgttcctta	552
Ser	Cys	Lys	Asn	Ala					
				140					

cttgtgctcc	ttccctatag	tgtttcatct	cgcagaagg	tgctccggct	ctggagggca	612
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ccgccagtgt	gtttgcacca	ggagacagta	aaggagctgc	tgcaggcagg	ttctgcacat	672
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ctgaacagct	gtcccctggc	tccactcttc	ttgcagtacc	tgccatgcct	tgctcaatta	732
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<211> 140

<212> PRT

<213> Mus musculus

<400> 51

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Pro	Glu	Glu	Ala	Asp	Ala	Asn	Glu	Glu	Gly	Val	Arg	Arg	Ala	Leu	Asp
		35					40					45			

Phe	Ala	Val	Ser	Glu	Tyr	Asn	Lys	Gly	Ser	Asn	Asp	Ala	Tyr	His	Ser
	50					55					60				

Arg	Ala	Ile	Gln	Val	Val	Arg	Ala	Arg	Lys	Gln	Leu	Val	Ala	Gly	Val
65					70					75					80

Asn Tyr Phe Leu Asp Val Glu Met Gly Arg Thr Thr Cys Thr Lys Ser
85 90 95

Gln Thr Asn Leu Thr Asp Cys Pro Phe His Asp Gln Pro His Leu Met
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Arg Lys Ala Leu Cys Ser Phe Gln Ile Tyr Ser Val Pro Trp Lys Gly
115 120 125

Thr His Ser Leu Thr Lys Phe Ser Cys Lys Asn Ala
130 135 140

<210> 52
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(513)
<223> SF11, cDNA: NM_000099, Protein: NP_000090

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gcgtcctagc cgacc atg gcc ggg ccc ctg cgc gcc ccg ctg ctc ctg ctg 111
Met Ala Gly Pro Leu Arg Ala Pro Leu Leu Leu Leu
1 5 10
gcc atc ctg gcc gtg gcc ctg gcc gtg agc ccc gcg gcc ggc tcc agt 159
Ala Ile Leu Ala Val Ala Leu Ala Val Ser Pro Ala Ala Gly Ser Ser
15 20 25
ccc ggc aag ccg ccg cgc ctg gtg gga ggc ccc atg gac gcc agc gtg 207
Pro Gly Lys Pro Pro Arg Leu Val Gly Gly Pro Met Asp Ala Ser Val
30 35 40
gag gag gag ggt gtg cgg cgt gca ctg gac ttt gcc gtc ggc gag tac 255
Glu Glu Glu Gly Val Arg Arg Ala Leu Asp Phe Ala Val Gly Glu Tyr
45 50 55 60
aac aaa gcc agc aac gac atg tac cac agc cgc gcg ctg cag gtg gtg 303
Asn Lys Ala Ser Asn Asp Met Tyr His Ser Arg Ala Leu Gln Val Val
65 70 75
cgc gcc cgc aag cag atc gta gct ggg gtg aac tac ttc ttg gac gtg 351
Arg Ala Arg Lys Gln Ile Val Ala Gly Val Asn Tyr Phe Leu Asp Val
80 85 90

gag ctg ggc cga acc acg tgt acc aag acc cag ccc aac ttg gac aac	399
Glu Leu Gly Arg Thr Thr Cys Thr Lys Thr Gln Pro Asn Leu Asp Asn	
95 100 105	
tgc ccc ttc cat gac cag cca cat ctg aaa agg aaa gca ttc tgc tct	447
Cys Pro Phe His Asp Gln Pro His Leu Lys Arg Lys Ala Phe Cys Ser	
110 115 120	
ttc cag atc tac gct gtg cct tgg cag ggc aca atg acc ttg tcg aaa	495
Phe Gln Ile Tyr Ala Val Pro Trp Gln Gly Thr Met Thr Leu Ser Lys	
125 130 135 140	
tcc acc tgt cag gac gcc taggggtctg taccgggctg gcctgtgcct	543
Ser Thr Cys Gln Asp Ala	
145	
atcacctctt atgcacacct cccaccccct gtattcccac ccctggactg gtggcccctg	603
ccttggggaa ggtctcccca tgtgcttgca ccaggagaca gacagagaag gcagcaggcg	663
gcctttgttg ctcagcaagg ggctctgccc tccctccttc cttcttgctt ctcataagccc	723
cggtgtgcgg tgcatacacc cccacctcct gcaataaaaat agtagcatcg gcaaaaaaaaa	783
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	818

<210> 53
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 53

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Val Ala Leu Ala Val Ser Pro Ala Ala Gly Ser Ser Pro Gly Lys Pro
20 25 30

Pro Arg Leu Val Gly Gly Pro Met Asp Ala Ser Val Glu Glu Glu Gly
35 40 45

Val Arg Arg Ala Leu Asp Phe Ala Val Gly Glu Tyr Asn Lys Ala Ser
50 55 60

Asn Asp Met Tyr His Ser Arg Ala Leu Gln Val Val Arg Ala Arg Lys
65 70 75 80

Gln Ile Val Ala Gly Val Asn Tyr Phe Leu Asp Val Glu Leu Gly Arg
85 90 95

Thr Thr Cys Thr Lys Thr Gln Pro Asn Leu Asp Asn Cys Pro Phe His
100 105 110

Asp Gln Pro His Leu Lys Arg Lys Ala Phe Cys Ser Phe Gln Ile Tyr
115 120 125

Ala Val Pro Trp Gln Gly Thr Met Thr Leu Ser Lys Ser Thr Cys Gln
130 135 140

Asp Ala
145

<210> 54
<211> 2709
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (124)..(2238)
<223> SF12, cDNA: NM_010180, Protein: NP_034310

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ccc atg gag cgc ccc gtg ccg tcg cgc ctc gtc ccg ctg ccg ctg ctg 168
Met Glu Arg Pro Val Pro Ser Arg Leu Val Pro Leu Pro Leu Leu
1 5 10 15
ctg ctc agc agc ctc tcg ctg ctg gca gcc cga gcg aat gca gac atc 216
Leu Leu Ser Ser Leu Ser Leu Leu Ala Ala Arg Ala Asn Ala Asp Ile
20 25 30
tcc atg gag gct tgc tgc acg gat cca aat cag atg gct aac cag cac 264
Ser Met Glu Ala Cys Cys Thr Asp Pro Asn Gln Met Ala Asn Gln His
35 40 45
agg gac tgc tcg ctg ccg tac acc tca gaa tcc aag gag tgc agg atg 312
Arg Asp Cys Ser Leu Pro Tyr Thr Ser Glu Ser Lys Glu Cys Arg Met
50 55 60
gtc cag gag caa tgt tgt cac aac caa ctg gaa gag ctg cac tgt gcc 360
Val Gln Glu Gln Cys Cys His Asn Gln Leu Glu Glu Leu His Cys Ala
65 70 75

acg ggc atc aac ctg gcc agc gag cca gaa ggc tgc gcc tcg ctc cac	408
Thr Gly Ile Asn Leu Ala Ser Glu Pro Glu Gly Cys Ala Ser Leu His	
80 85 90 95	
agc tac aac agt agc ctt gag acc atc ttc ata aag agg tgc tgc cac	456
Ser Tyr Asn Ser Ser Leu Glu Thr Ile Phe Ile Lys Arg Cys Cys His	
100 105 110	
tgt tgc atg ctg gga aag gca tcc ctg gcc cga gac cag acc tgt gaa	504
Cys Cys Met Leu Gly Lys Ala Ser Leu Ala Arg Asp Gln Thr Cys Glu	
115 120 125	
ccc att gtc atg ata agc tac cag tgt ggg ctg gtg ttc cgt gcc tgc	552
Pro Ile Val Met Ile Ser Tyr Gln Cys Gly Leu Val Phe Arg Ala Cys	
130 135 140	
tgt gtg aag gcc cgg gag aat tca gac ttt gtc caa ggc aac ggt gca	600
Cys Val Lys Ala Arg Glu Asn Ser Asp Phe Val Gln Gly Asn Gly Ala	
145 150 155	
gac ctt cag gac cca gct aag att cct gac gag gag gac caa gaa gac	648
Asp Leu Gln Asp Pro Ala Lys Ile Pro Asp Glu Glu Asp Gln Glu Asp	
160 165 170 175	
ccg tac ctg aat gac cgc tgt cga ggt ggc ggg ccc tgt aag cag cag	696
Pro Tyr Leu Asn Asp Arg Cys Arg Gly Gly Gly Pro Cys Lys Gln Gln	
180 185 190	
tgc cgt gac act ggg gac gag gtg atc tgc tct tgc ttt gtg ggc tac	744
Cys Arg Asp Thr Gly Asp Glu Val Ile Cys Ser Cys Phe Val Gly Tyr	
195 200 205	
cag ctg cag tcg gat ggt gtc tcc tgc gaa gat atc aat gaa tgc atc	792
Gln Leu Gln Ser Asp Gly Val Ser Cys Glu Asp Ile Asn Glu Cys Ile	
210 215 220	
aca ggc agc cat aac tgc cgg ctg gga gaa tcc tgc atc aat aca gtg	840
Thr Gly Ser His Asn Cys Arg Leu Gly Glu Ser Cys Ile Asn Thr Val	
225 230 235	
ggc tct ttc cgc tgc cag cgg gac agc agc tgt ggg act ggc tat gag	888
Gly Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly Thr Gly Tyr Glu	
240 245 250 255	
ctc aca gag gat aat aac tgc aaa gat att gac gaa tgt gag act ggt	936
Leu Thr Glu Asp Asn Asn Cys Lys Asp Ile Asp Glu Cys Glu Thr Gly	
260 265 270	
att cat aac tgc ccc ccc gat ttt atc tgt cag aat act ctg gga tcc	984
Ile His Asn Cys Pro Pro Asp Phe Ile Cys Gln Asn Thr Leu Gly Ser	
275 280 285	
ttc cgt tgc aga ccg aag ctg cag tgc aag agc ggc ttc ata cag gat	1032
Phe Arg Cys Arg Pro Lys Leu Gln Cys Lys Ser Gly Phe Ile Gln Asp	

290					295					300						
gct	cta	ggc	aac	tgc	att	gat	atc	aat	gag	tgt	tta	agt	atc	agt	gct	1080
Ala	Leu	Gly	Asn	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Leu	Ser	Ile	Ser	Ala	
	305					310					315					
cca	tgc	cct	gtg	ggg	cag	aca	tgc	atc	aat	aca	gag	ggc	tcc	tac	aca	1128
Pro	Cys	Pro	Val	Gly	Gln	Thr	Cys	Ile	Asn	Thr	Glu	Gly	Ser	Tyr	Thr	
320					325					330					335	
tgc	cag	aag	aat	gtg	ccc	aac	tgt	ggc	cgt	ggc	tat	cat	ctc	aat	gaa	1176
Cys	Gln	Lys	Asn	Val	Pro	Asn	Cys	Gly	Arg	Gly	Tyr	His	Leu	Asn	Glu	
				340					345					350		
gag	ggg	acc	cgc	tgt	gtt	gat	gtg	gat	gag	tgc	gcc	cca	cca	gcg	gag	1224
Glu	Gly	Thr	Arg	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Pro	Pro	Ala	Glu	
			355					360					365			
ccc	tgt	ggg	aag	gga	cac	cac	tgc	ctg	aac	tcc	ccc	ggc	agc	ttc	cgc	1272
Pro	Cys	Gly	Lys	Gly	His	His	Cys	Leu	Asn	Ser	Pro	Gly	Ser	Phe	Arg	
		370					375					380				
tgc	gag	tgc	aag	gct	ggc	ttc	tat	ttt	gat	ggc	atc	agc	agg	acc	tgc	1320
Cys	Glu	Cys	Lys	Ala	Gly	Phe	Tyr	Phe	Asp	Gly	Ile	Ser	Arg	Thr	Cys	
	385					390					395					
gtg	gat	atc	aac	gag	tgc	cag	cgc	tat	ccc	ggg	cgc	ctg	tgt	ggc	cac	1368
Val	Asp	Ile	Asn	Glu	Cys	Gln	Arg	Tyr	Pro	Gly	Arg	Leu	Cys	Gly	His	
400					405					410					415	
aag	tgt	gag	aac	acg	cca	ggc	tcc	ttc	cac	tgc	agc	tgc	tcc	gcc	ggc	1416
Lys	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Phe	His	Cys	Ser	Cys	Ser	Ala	Gly	
				420					425					430		
ttc	cgg	ctg	tct	gtg	gac	ggc	cgg	tct	tgt	gaa	gat	gtg	aac	gag	tgt	1464
Phe	Arg	Leu	Ser	Val	Asp	Gly	Arg	Ser	Cys	Glu	Asp	Val	Asn	Glu	Cys	
			435					440					445			
ctc	aac	agc	cct	tgc	agc	cag	gag	tgt	gct	aat	gtc	tat	ggc	tcc	tac	1512
Leu	Asn	Ser	Pro	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Val	Tyr	Gly	Ser	Tyr	
		450					455					460				
cag	tgc	tat	tgc	cga	cga	ggc	tac	cag	ctc	agt	gac	gtg	gat	ggg	gtc	1560
Gln	Cys	Tyr	Cys	Arg	Arg	Gly	Tyr	Gln	Leu	Ser	Asp	Val	Asp	Gly	Val	
	465					470					475					
acc	tgc	gaa	gat	att	gat	gag	tgt	gcc	ctg	ccc	act	gga	ggc	cac	atc	1608
Thr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ala	Leu	Pro	Thr	Gly	Gly	His	Ile	
480					485					490					495	
tgc	tcc	tac	cgc	tgc	atc	aac	atc	ccc	gga	agc	ttc	cag	tgc	agc	tgc	1656
Cys	Ser	Tyr	Arg	Cys	Ile	Asn	Ile	Pro	Gly	Ser	Phe	Gln	Cys	Ser	Cys	
				500					505					510		
ccc	tca	tct	ggc	tac	agg	cta	gct	ccc	aat	ggc	cgc	aac	tgc	caa	gac	1704

Pro	Ser	Ser	Gly	Tyr	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asn	Cys	Gln	Asp	
			515					520					525			
att	gat	gag	tgt	gtg	acc	ggc	atc	cat	aac	tgt	tcc	atc	aat	gag	act	1752
Ile	Asp	Glu	Cys	Val	Thr	Gly	Ile	His	Asn	Cys	Ser	Ile	Asn	Glu	Thr	
		530					535					540				
tgc	ttc	aac	atc	cag	ggc	agc	ttc	cgc	tgt	ctg	tcc	ttt	gaa	tgc	ccc	1800
Cys	Phe	Asn	Ile	Gln	Gly	Ser	Phe	Arg	Cys	Leu	Ser	Phe	Glu	Cys	Pro	
	545					550					555					
gag	aac	tat	cgc	cgc	tcc	gca	gac	acc	ttc	cgc	caa	gag	aaa	aca	gac	1848
Glu	Asn	Tyr	Arg	Arg		Ala	Asp	Thr	Phe	Arg	Gln	Glu	Lys	Thr	Asp	
560					565					570					575	
acc	gtc	cgc	tgc	atc	aag	tct	tgc	cgt	ccc	aac	gat	gag	gcc	tgc	gtg	1896
Thr	Val	Arg	Cys	Ile	Lys	Ser	Cys	Arg	Pro	Asn	Asp	Glu	Ala	Cys	Val	
				580					585					590		
cgg	gac	cct	gta	cat	acc	gtc	tcc	cac	acc	gtc	atc	tcg	ctg	ccc	acc	1944
Arg	Asp	Pro	Val	His	Thr	Val	Ser	His	Thr	Val	Ile	Ser	Leu	Pro	Thr	
			595					600					605			
ttt	cga	gag	ttc	acc	cgt	cct	gag	gag	atc	atc	ttt	ctg	agg	gct	gtc	1992
Phe	Arg	Glu	Phe	Thr	Arg	Pro	Glu	Glu	Ile	Ile	Phe	Leu	Arg	Ala	Val	
		610					615					620				
aca	ccg	ctg	tac	ccc	gcc	aac	cag	gcc	gac	atc	atc	ttc	gac	atc	aca	2040
Thr	Pro	Leu	Tyr	Pro	Ala	Asn	Gln	Ala	Asp	Ile	Ile	Phe	Asp	Ile	Thr	
	625					630					635					
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Glu	Gly	Asn	Leu	Arg	Asp	Ser	Phe	Asp	Ile	Ile	Lys	Arg	Tyr	Glu	Asp	
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Gly	Met	Thr	Val	Gly	Val	Val	Arg	Gln	Val	Arg	Pro	Ile	Val	Gly	Pro	
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ttt	tac	gct	gtc	ctg	aag	ctg	gag	atg	aac	tac	gtg	ttg	gga	ggc	gta	2184
Phe	Tyr	Ala	Val	Leu	Lys	Leu	Glu	Met	Asn	Tyr	Val	Leu	Gly	Gly	Val	
			675					680					685			
gtt	tcc	cac	cgg	aac	gtc	gtc	aat	gta	cac	atc	ttc	gtc	tcc	gag	tac	2232
Val	Ser	His	Arg	Asn	Val	Val	Asn	Val	His	Ile	Phe	Val	Ser	Glu	Tyr	
		690					695					700				
tgg	ttc	tgagggccgg	ggtg	gcggctc	agccaggagt	gtgccacgcc	cttgctgcca									2288
Trp	Phe															
	705															
gtgacagcca	ggtgcctgtc	tctaccacctc	gggcctccct	tgatgtttca	tattggtttg											2348
tatggccacg	tgcattaggc	tgagccgaat	cacttaagtc	cagctggtgt	actgtggcgt											2408

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 a 2709

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 35 40 45

Asp Cys Ser Leu Pro Tyr Thr Ser Glu Ser Lys Glu Cys Arg Met Val
 50 55 60

Gln Glu Gln Cys Cys His Asn Gln Leu Glu Glu Leu His Cys Ala Thr
 65 70 75 80

Gly Ile Asn Leu Ala Ser Glu Pro Glu Gly Cys Ala Ser Leu His Ser
 85 90 95

Tyr Asn Ser Ser Leu Glu Thr Ile Phe Ile Lys Arg Cys Cys His Cys
 100 105 110

Cys Met Leu Gly Lys Ala Ser Leu Ala Arg Asp Gln Thr Cys Glu Pro
 115 120 125

Ile Val Met Ile Ser Tyr Gln Cys Gly Leu Val Phe Arg Ala Cys Cys
 130 135 140

Val	Lys	Ala	Arg	Glu	Asn	Ser	Asp	Phe	Val	Gln	Gly	Asn	Gly	Ala	Asp	
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Tyr	Leu	Asn	Asp	Arg	Cys	Arg	Gly	Gly	Gly	Pro	Cys	Lys	Gln	Gln	Cys	
			180					185					190			
Arg	Asp	Thr	Gly	Asp	Glu	Val	Ile	Cys	Ser	Cys	Phe	Val	Gly	Tyr	Gln	
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Leu	Gln	Ser	Asp	Gly	Val	Ser	Cys	Glu	Asp	Ile	Asn	Glu	Cys	Ile	Thr	
	210					215					220					
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Ser	Phe	Arg	Cys	Gln	Arg	Asp	Ser	Ser	Cys	Gly	Thr	Gly	Tyr	Glu	Leu	
				245					250					255		
Thr	Glu	Asp	Asn	Asn	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Glu	Thr	Gly	Ile	
			260					265					270			
His	Asn	Cys	Pro	Pro	Asp	Phe	Ile	Cys	Gln	Asn	Thr	Leu	Gly	Ser	Phe	
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Arg	Cys	Arg	Pro	Lys	Leu	Gln	Cys	Lys	Ser	Gly	Phe	Ile	Gln	Asp	Ala	
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Leu	Gly	Asn	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Leu	Ser	Ile	Ser	Ala	Pro	
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Cys	Pro	Val	Gly	Gln	Thr	Cys	Ile	Asn	Thr	Glu	Gly	Ser	Tyr	Thr	Cys	
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Gln	Lys	Asn	Val	Pro	Asn	Cys	Gly	Arg	Gly	Tyr	His	Leu	Asn	Glu	Glu	
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Gly	Thr	Arg	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Pro	Pro	Ala	Glu	Pro	
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Cys Gly Lys Gly His His Cys Leu Asn Ser Pro Gly Ser Phe Arg Cys
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Glu Cys Lys Ala Gly Phe Tyr Phe Asp Gly Ile Ser Arg Thr Cys Val
 385 390 395 400

Asp Ile Asn Glu Cys Gln Arg Tyr Pro Gly Arg Leu Cys Gly His Lys
 405 410 415

Cys Glu Asn Thr Pro Gly Ser Phe His Cys Ser Cys Ser Ala Gly Phe
 420 425 430

Arg Leu Ser Val Asp Gly Arg Ser Cys Glu Asp Val Asn Glu Cys Leu
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Asn Ser Pro Cys Ser Gln Glu Cys Ala Asn Val Tyr Gly Ser Tyr Gln
 450 455 460

Cys Tyr Cys Arg Arg Gly Tyr Gln Leu Ser Asp Val Asp Gly Val Thr
 465 470 475 480

Cys Glu Asp Ile Asp Glu Cys Ala Leu Pro Thr Gly Gly His Ile Cys
 485 490 495

Ser Tyr Arg Cys Ile Asn Ile Pro Gly Ser Phe Gln Cys Ser Cys Pro
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Ser Ser Gly Tyr Arg Leu Ala Pro Asn Gly Arg Asn Cys Gln Asp Ile
 515 520 525

Asp Glu Cys Val Thr Gly Ile His Asn Cys Ser Ile Asn Glu Thr Cys
 530 535 540

Phe Asn Ile Gln Gly Ser Phe Arg Cys Leu Ser Phe Glu Cys Pro Glu
 545 550 555 560

Asn Tyr Arg Arg Ser Ala Asp Thr Phe Arg Gln Glu Lys Thr Asp Thr
 565 570 575

Val Arg Cys Ile Lys Ser Cys Arg Pro Asn Asp Glu Ala Cys Val Arg

580	585	590
Asp Pro Val His Thr Val Ser His Thr Val Ile Ser Leu Pro Thr Phe		
595	600	605
Arg Glu Phe Thr Arg Pro Glu Glu Ile Ile Phe Leu Arg Ala Val Thr		
610	615	620
Pro Leu Tyr Pro Ala Asn Gln Ala Asp Ile Ile Phe Asp Ile Thr Glu		
625	630	635
Gly Asn Leu Arg Asp Ser Phe Asp Ile Ile Lys Arg Tyr Glu Asp Gly		
645	650	655
Met Thr Val Gly Val Val Arg Gln Val Arg Pro Ile Val Gly Pro Phe		
660	665	670
Tyr Ala Val Leu Lys Leu Glu Met Asn Tyr Val Leu Gly Gly Val Val		
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Ser His Arg Asn Val Val Asn Val His Ile Phe Val Ser Glu Tyr Trp		
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Phe
705

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ccgcccaccg cccgtcgccc gccgccc atg gag cgc gcc gcg ccg tcg cgc cgg	174
Met Glu Arg Ala Ala Pro Ser Arg Arg	
1 5	

gtc	ccg	ctt	ccg	ctg	ctg	ctg	ctc	ggc	ggc	ctt	gcg	ctg	ctg	gcg	gcc	222
Val	Pro	Leu	Pro	Leu	Leu	Leu	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Ala	Ala	
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gga	gtg	gac	gcg	gat	gtc	ctc	ctg	gag	gcc	tgc	tgt	gcg	gac	gga	cac	270
Gly	Val	Asp	Ala	Asp	Val	Leu	Leu	Glu	Ala	Cys	Cys	Ala	Asp	Gly	His	
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cgg	atg	gcc	act	cat	cag	aag	gac	tgc	tcg	ctg	cca	tat	gct	acg	gaa	318
Arg	Met	Ala	Thr	His	Gln	Lys	Asp	Cys	Ser	Leu	Pro	Tyr	Ala	Thr	Glu	
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tcc	aaa	gaa	tgc	agg	atg	gtg	cag	gag	cag	tgc	tgc	cac	agc	cag	ctg	366
Ser	Lys	Glu	Cys	Arg	Met	Val	Gln	Glu	Gln	Cys	Cys	His	Ser	Gln	Leu	
		60					65					70				
gag	gag	ctg	cac	tgt	gcc	acg	ggc	atc	agc	ctg	gcc	aac	gag	cag	gac	414
Glu	Glu	Leu	His	Cys	Ala	Thr	Gly	Ile	Ser	Leu	Ala	Asn	Glu	Gln	Asp	
	75					80					85					
cgc	tgt	gcc	acg	ccc	cac	ggt	gac	aac	gcc	agc	ctg	gag	gcc	aca	ttt	462
Arg	Cys	Ala	Thr	Pro	His	Gly	Asp	Asn	Ala	Ser	Leu	Glu	Ala	Thr	Phe	
90					95					100					105	
gtg	aag	agg	tgc	tgc	cat	tgc	tgt	ctg	ctg	ggg	agg	gcg	gcc	cag	gcc	510
Val	Lys	Arg	Cys	Cys	His	Cys	Cys	Leu	Leu	Gly	Arg	Ala	Ala	Gln	Ala	
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Gln	Gly	Gln	Ser	Cys	Glu	Tyr	Ser	Leu	Met	Val	Gly	Tyr	Gln	Cys	Gly	
			125					130					135			
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Gln	Val	Phe	Arg	Ala	Cys	Cys	Val	Lys	Ser	Gln	Glu	Thr	Gly	Asp	Leu	
		140					145					150				
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Asp	Val	Gly	Gly	Leu	Gln	Glu	Thr	Asp	Lys	Ile	Ile	Glu	Val	Glu	Glu	
	155					160					165					
gaa	caa	gag	gac	cca	tat	ctg	aat	gac	cgc	tgc	cga	gga	ggc	ggg	ccc	702
Glu	Gln	Glu	Asp	Pro	Tyr	Leu	Asn	Asp	Arg	Cys	Arg	Gly	Gly	Gly	Pro	
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Cys	Lys	Gln	Gln	Cys	Arg	Asp	Thr	Gly	Asp	Glu	Val	Val	Cys	Ser	Cys	
				190					195					200		
ttc	gtg	ggc	tac	cag	ctg	ctg	tct	gat	ggt	gtc	tcc	tgt	gaa	gat	gtc	798
Phe	Val	Gly	Tyr	Gln	Leu	Leu	Ser	Asp	Gly	Val	Ser	Cys	Glu	Asp	Val	
			205					210					215			
aat	gaa	tgc	atc	acg	ggc	agc	cac	agc	tgc	cgg	ctt	gga	gaa	tcc	tgc	846
Asn	Glu	Cys	Ile	Thr	Gly	Ser	His	Ser	Cys	Arg	Leu	Gly	Glu	Ser	Cys	
		220					225					230				

atc aac aca gtg ggc tct ttc cgc tgc cag cgg gac agc agc tgc ggg Ile Asn Thr Val Gly Ser Phe Arg Cys Gln Arg Asp Ser Ser Cys Gly 235 240 245	894
act ggc tat gag ctc aca gag gac aat agc tgc aaa gat att gac gag Thr Gly Tyr Glu Leu Thr Glu Asp Asn Ser Cys Lys Asp Ile Asp Glu 250 255 260 265	942
tgt gag agt ggt att cat aac tgc ctc ccc gat ttt atc tgt cag aat Cys Glu Ser Gly Ile His Asn Cys Leu Pro Asp Phe Ile Cys Gln Asn 270 275 280	990
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ggc tcc tac acg tgc cag aag aac gtg ccc aac tgt ggc cgt ggc tac Gly Ser Tyr Thr Cys Gln Lys Asn Val Pro Asn Cys Gly Arg Gly Tyr 330 335 340 345	1182
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cca cct gct gag ccc tgt ggg aag gga cat cgc tgc gtg aac tct ccc Pro Pro Ala Glu Pro Cys Gly Lys Gly His Arg Cys Val Asn Ser Pro 365 370 375	1278
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445						450						455						
tac	ggc	tcc	tac	cag	tgt	tac	tgc	cgg	cga	ggc	tac	cag	ctc	agc	gat	1566		
Tyr	Gly	Ser	Tyr	Gln	Cys	Tyr	Cys	Arg	Arg	Gly	Tyr	Gln	Leu	Ser	Asp			
		460					465					470						
gtg	gat	gga	gtc	acc	tgt	gaa	gac	atc	gac	gag	tgc	gcc	ctg	ccc	acc	1614		
Val	Asp	Gly	Val	Thr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ala	Leu	Pro	Thr			
	475					480					485							
ggg	ggc	cac	atc	tgc	tcc	tac	cgc	tgc	atc	aac	atc	cct	gga	agc	ttc	1662		
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cag	tgc	agc	tgc	ccc	tcg	tct	ggc	tac	agg	ctg	gcc	ccc	aat	ggc	cgc	1710		
Gln	Cys	Ser	Cys	Pro	Ser	Ser	Gly	Tyr	Arg	Leu	Ala	Pro	Asn	Gly	Arg			
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aac	tgc	caa	gac	att	gat	gag	tgt	gtg	act	ggc	atc	cac	aac	tgc	tcc	1758		
Asn	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Val	Thr	Gly	Ile	His	Asn	Cys	Ser			
			525					530					535					
atc	aac	gag	acc	tgc	ttc	aac	atc	cag	ggc	ggc	ttc	cgc	tgc	ctg	gcc	1806		
Ile	Asn	Glu	Thr	Cys	Phe	Asn	Ile	Gln	Gly	Gly	Phe	Arg	Cys	Leu	Ala			
		540					545					550						
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Phe	Glu	Cys	Pro	Glu	Asn	Tyr	Arg	Arg	Ser	Ala	Ala	Thr	Leu	Gln	Gln			
	555					560					565							
gag	aag	aca	gac	acg	gtc	cgc	tgc	atc	aag	tcc	tgc	cgc	ccc	aac	gat	1902		
Glu	Lys	Thr	Asp	Thr	Val	Arg	Cys	Ile	Lys	Ser	Cys	Arg	Pro	Asn	Asp			
570					575					580					585			
gtc	aca	tgc	gtg	ttc	gac	ccc	gtg	cac	acc	atc	tcc	cac	acc	gtc	atc	1950		
Val	Thr	Cys	Val	Phe	Asp	Pro	Val	His	Thr	Ile	Ser	His	Thr	Val	Ile			
				590					595					600				
tcg	ctg	cct	acc	ttc	cgc	gag	ttc	acc	cgc	cct	gaa	gag	atc	atc	ttc	1998		
Ser	Leu	Pro	Thr	Phe	Arg	Glu	Phe	Thr	Arg	Pro	Glu	Glu	Ile	Ile	Phe			
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Leu	Arg	Ala	Ile	Thr	Pro	Pro	His	Pro	Ala	Ser	Gln	Ala	Asn	Ile	Ile			
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ttc	gac	atc	acg	gaa	ggg	aac	ctg	cgg	gac	tct	ttt	gac	atc	atc	aag	2094		
Phe	Asp	Ile	Thr	Glu	Gly	Asn	Leu	Arg	Asp	Ser	Phe	Asp	Ile	Ile	Lys			
	635					640					645							
cgt	tac	atg	gac	ggc	atg	acc	gtg	ggg	gtc	gtg	cgc	cag	gtg	cgg	ccc	2142		
Arg	Tyr	Met	Asp	Gly	Met	Thr	Val	Gly	Val	Val	Arg	Gln	Val	Arg	Pro			
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atc	gtg	ggc	cca	ttt	cat	gcc	gtc	ctg	aag	ctg	gag	atg	aac	tat	gtg	2190		

Ile	Val	Gly	Pro	Phe	His	Ala	Val	Leu	Lys	Leu	Glu	Met	Asn	Tyr	Val		
				670					675						680		
gtc	ggg	ggc	gtg	gtc	tcc	cac	cga	aat	ggt	gtc	aac	gtc	cac	atc	ttc		2238
Val	Gly	Gly	Val	Val	Ser	His	Arg	Asn	Val	Val	Asn	Val	His	Ile	Phe		
			685					690					695				
gtc	tct	gag	tac	tgg	ttc	tgagggctgg	tctgccgcac	agccgcaggt									2286
Val	Ser	Glu	Tyr	Trp	Phe												
			700														
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<400> 57

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			20					25					30				

Leu	Glu	Ala	Cys	Cys	Ala	Asp	Gly	His	Arg	Met	Ala	Thr	His	Gln	Lys		
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Asp	Cys	Ser	Leu	Pro	Tyr	Ala	Thr	Glu	Ser	Lys	Glu	Cys	Arg	Met	Val
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Gln	Glu	Gln	Cys	Cys	His	Ser	Gln	Leu	Glu	Glu	Leu	His	Cys	Ala	Thr
65					70					75					80
Gly	Ile	Ser	Leu	Ala	Asn	Glu	Gln	Asp	Arg	Cys	Ala	Thr	Pro	His	Gly
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Asp	Asn	Ala	Ser	Leu	Glu	Ala	Thr	Phe	Val	Lys	Arg	Cys	Cys	His	Cys
			100					105					110		
Cys	Leu	Leu	Gly	Arg	Ala	Ala	Gln	Ala	Gln	Gly	Gln	Ser	Cys	Glu	Tyr
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Ser	Leu	Met	Val	Gly	Tyr	Gln	Cys	Gly	Gln	Val	Phe	Arg	Ala	Cys	Cys
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Val	Lys	Ser	Gln	Glu	Thr	Gly	Asp	Leu	Asp	Val	Gly	Gly	Leu	Gln	Glu
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Thr	Asp	Lys	Ile	Ile	Glu	Val	Glu	Glu	Glu	Gln	Glu	Asp	Pro	Tyr	Leu
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Asn	Asp	Arg	Cys	Arg	Gly	Gly	Gly	Pro	Cys	Lys	Gln	Gln	Cys	Arg	Asp
			180					185					190		
Thr	Gly	Asp	Glu	Val	Val	Cys	Ser	Cys	Phe	Val	Gly	Tyr	Gln	Leu	Leu
		195					200					205			
Ser	Asp	Gly	Val	Ser	Cys	Glu	Asp	Val	Asn	Glu	Cys	Ile	Thr	Gly	Ser
	210					215					220				
His	Ser	Cys	Arg	Leu	Gly	Glu	Ser	Cys	Ile	Asn	Thr	Val	Gly	Ser	Phe
225					230					235					240
Arg	Cys	Gln	Arg	Asp	Ser	Ser	Cys	Gly	Thr	Gly	Tyr	Glu	Leu	Thr	Glu
				245					250					255	
Asp	Asn	Ser	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ile	His	Asn
			260					265					270		

Cys Leu Pro Asp Phe Ile Cys Gln Asn Thr Leu Gly Ser Phe Arg Cys
 275 280 285

Arg Pro Lys Leu Gln Cys Lys Ser Gly Phe Ile Gln Asp Ala Leu Gly
 290 295 300

Asn Cys Ile Asp Ile Asn Glu Cys Leu Ser Ile Ser Ala Pro Cys Pro
 305 310 315 320

Ile Gly His Thr Cys Ile Asn Thr Glu Gly Ser Tyr Thr Cys Gln Lys
 325 330 335

Asn Val Pro Asn Cys Gly Arg Gly Tyr His Leu Asn Glu Glu Gly Thr
 340 345 350

Arg Cys Val Asp Val Asp Glu Cys Ala Pro Pro Ala Glu Pro Cys Gly
 355 360 365

Lys Gly His Arg Cys Val Asn Ser Pro Gly Ser Phe Arg Cys Glu Cys
 370 375 380

Lys Thr Gly Tyr Tyr Phe Asp Gly Ile Ser Arg Met Cys Val Asp Val
 385 390 395 400

Asn Glu Cys Gln Arg Tyr Pro Gly Arg Leu Cys Gly His Lys Cys Glu
 405 410 415

Asn Thr Leu Gly Ser Tyr Leu Cys Ser Cys Ser Val Gly Phe Arg Leu
 420 425 430

Ser Val Asp Gly Arg Ser Cys Glu Asp Ile Asn Glu Cys Ser Ser Ser
 435 440 445

Pro Cys Ser Gln Glu Cys Ala Asn Val Tyr Gly Ser Tyr Gln Cys Tyr
 450 455 460

Cys Arg Arg Gly Tyr Gln Leu Ser Asp Val Asp Gly Val Thr Cys Glu
 465 470 475 480

Asp Ile Asp Glu Cys Ala Leu Pro Thr Gly Gly His Ile Cys Ser Tyr
 485 490 495

Arg Cys Ile Asn Ile Pro Gly Ser Phe Gln Cys Ser Cys Pro Ser Ser
500 505 510

Gly Tyr Arg Leu Ala Pro Asn Gly Arg Asn Cys Gln Asp Ile Asp Glu
515 520 525

Cys Val Thr Gly Ile His Asn Cys Ser Ile Asn Glu Thr Cys Phe Asn
530 535 540

Ile Gln Gly Gly Phe Arg Cys Leu Ala Phe Glu Cys Pro Glu Asn Tyr
545 550 555 560

Arg Arg Ser Ala Ala Thr Leu Gln Gln Glu Lys Thr Asp Thr Val Arg
565 570 575

Cys Ile Lys Ser Cys Arg Pro Asn Asp Val Thr Cys Val Phe Asp Pro
580 585 590

Val His Thr Ile Ser His Thr Val Ile Ser Leu Pro Thr Phe Arg Glu
595 600 605

Phe Thr Arg Pro Glu Glu Ile Ile Phe Leu Arg Ala Ile Thr Pro Pro
610 615 620

His Pro Ala Ser Gln Ala Asn Ile Ile Phe Asp Ile Thr Glu Gly Asn
625 630 635 640

Leu Arg Asp Ser Phe Asp Ile Ile Lys Arg Tyr Met Asp Gly Met Thr
645 650 655

Val Gly Val Val Arg Gln Val Arg Pro Ile Val Gly Pro Phe His Ala
660 665 670

Val Leu Lys Leu Glu Met Asn Tyr Val Val Gly Gly Val Val Ser His
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Arg Asn Val Val Asn Val His Ile Phe Val Ser Glu Tyr Trp Phe
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 Met Leu Arg Leu Ser Glu
 1 5
 cgc aat atg aag gtg ctc ttc gcc gcc gcc ctc atc gtg ggc tcc gtc 163
 Arg Asn Met Lys Val Leu Phe Ala Ala Ala Leu Ile Val Gly Ser Val
 10 15 20
 gtc ttc ctt ttg ctg ccc gga ccc tcc gtg gcc aac gat aag aag aag 211
 Val Phe Leu Leu Leu Pro Gly Pro Ser Val Ala Asn Asp Lys Lys Lys
 25 30 35
 gga cct aaa gtc aca gtc aag gta tac ttt gat tta caa att gga gat 259
 Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Gln Ile Gly Asp
 40 45 50
 gaa tct gta gga cga gtc gtc ttt gga ctc ttt gga aag act gtt cca 307
 Glu Ser Val Gly Arg Val Val Phe Gly Leu Phe Gly Lys Thr Val Pro
 55 60 65 70
 aaa aca gtg gat aat ttt gta gcc tta gct aca gga gag aaa gga ttt 355
 Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly Phe
 75 80 85
 ggc tac aaa aac agc aag ttc cat cgt gtc atc aag gac ttc atg atc 403
 Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp Phe Met Ile
 90 95 100
 cag ggt gga gac ttc acc agg gga gat ggc aca gga gga aag agc atc 451
 Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly Lys Ser Ile
 105 110 115
 tat ggt gag cgc ttc cca gat gag aac ttc aag ctg aag cac tac ggg 499
 Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys His Tyr Gly
 120 125 130
 cct ggc tgg gtg agc atg gcc aat gca ggc aaa gac acc aat ggc tca 547
 Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr Asn Gly Ser
 135 140 145 150
 cag ttc ttc ata acc aca gtc aag acc tcc tgg ctg gat ggc aag cat 595
 Gln Phe Phe Ile Thr Thr Val Lys Thr Ser Trp Leu Asp Gly Lys His

155										160					165					
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			170					175					180							
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Glu	Ser	Thr	Lys	Thr	Asp	Ser	Arg	Asp	Lys	Pro	Leu	Lys	Asp	Val	Ile					
		185					190					195								
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Ile	Val	Asp	Ser	Gly	Lys	Ile	Glu	Val	Glu	Lys	Pro	Phe	Ala	Ile	Ala					
	200					205					210									
aag	gag	tagagagcct	gggggacctc	atccctctaa	gcagctgtct	gtgtgggtcc	795													
Lys	Glu																			
215																				
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<400> 59

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			20					25					30		

Ala	Asn	Asp	Lys	Lys	Lys	Gly	Pro	Lys	Val	Thr	Val	Lys	Val	Tyr	Phe
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Asp	Leu	Gln	Ile	Gly	Asp	Glu	Ser	Val	Gly	Arg	Val	Val	Phe	Gly	Leu
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Phe	Gly	Lys	Thr	Val	Pro	Lys	Thr	Val	Asp	Asn	Phe	Val	Ala	Leu	Ala
65					70					75				80	

Thr	Gly	Glu	Lys	Gly	Phe	Gly	Tyr	Lys	Asn	Ser	Lys	Phe	His	Arg	Val
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85

90

95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
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Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
 115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
 130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ser
 145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
 165 170 175

Asp Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
 180 185 190

Pro Leu Lys Asp Val Ile Ile Val Asp Ser Gly Lys Ile Glu Val Glu
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Lys Pro Phe Ala Ile Ala Lys Glu
 210 215

<210> 60

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accctcttcc ggcctcagct gtccgggctg ctttcgcctc cgcctgtgg atg ctg cgc 178
 Met Leu Arg
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ctc tcc gaa cgc aac atg aag gtg ctc ctt gcc gcc gcc ctc atc gcg Leu Ser Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala Leu Ile Ala 5 10 15	226
ggg tcc gtc ttc ttc ctg ctg ctg ccg gga cct tct gcg gcc gat gag Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala Ala Asp Glu 20 25 30 35	274
aag aag aag ggg ccc aaa gtc acc gtc aag gtg tat ttt gac cta cga Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Arg 40 45 50	322
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act gtt cca aaa aca gtg gat aat ttt gtg gcc tta gct aca gga gag Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu 70 75 80	418
aaa gga ttt ggc tac aaa aac agc aaa ttc cat cgt gta atc aag gac Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp 85 90 95	466
ttc atg atc cag ggc gga gac ttc acc agg gga gat ggc aca gga gga Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly 100 105 110 115	514
aag agc atc tac ggt gag cgc ttc ccc gat gag aac ttc aaa ctg aag Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys 120 125 130	562
cac tac ggg cct ggc tgg gtg agc atg gcc aac gca ggc aaa gac acc His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr 135 140 145	610
aac ggc tcc cag ttc ttc atc acg aca gtc aag aca gcc tgg cta gat Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala Trp Leu Asp 150 155 160	658
ggc aag cat gtg gtg ttt ggc aaa gtt cta gag ggc atg gag gtg gtg Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met Glu Val Val 165 170 175	706
cgg aag gtg gag agc acc aag aca gac agc cgg gat aaa ccc ctg aag Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys Pro Leu Lys 180 185 190 195	754
gat gtg atc atc gca gac tgc ggc aag atc gag gtg gag aag ccc ttt Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu Lys Pro Phe 200 205 210	802
gcc atc gcc aag gag tagggcacag ggacatcttt ctttgagtga ccgtctgtgc Ala Ile Ala Lys Glu 215	857

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<210> 61
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<400> 61

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Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
 35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
 50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
 65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
 85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
 100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
 115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
 130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
 145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
210 215